

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 19:48:48 ; Search time 3017 Seconds
(without alignments)
8817.612 Million cell updates/sec

Title: US-10-327-713-267
Perfect score: 468
Sequence: 1 gactgagctgccttagtg.....ngncacacccgcctcatg 468

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	415	88.7	2962	9	BC015301	BC015301 Mus muscu
2	378.2	80.8	2851	9	BC085781	BC085781 Rattus no
3	316	67.5	2308	8	AK222911	AK222911 Homo sapi
4	316	67.5	2392	6	AX833134	AX833134 Sequence
5	316	67.5	2392	8	AK094636	AK094636 Homo sapi
6	316	67.5	2417	6	CQ717207	CQ717207 Sequence
7	316	67.5	2487	6	BD156975	BD156975 Primer fo
8	316	67.5	2487	6	AX878013	AX878013 Sequence
9	316	67.5	2487	8	AK002018	AK002018 Homo sapi
10	316	67.5	5089	6	CQ850926	CQ850926 Sequence
11	316	67.5	5089	8	AK128129	AK128129 Homo sapi
12	312.8	66.8	2417	8	AF047650	AF047650 Homo sapi
13	302.4	64.6	2383	6	BD160664	BD160664 Primer fo
14	302.4	64.6	2383	6	AX884014	AX884014 Sequence
15	302.4	64.6	2383	8	AK024401	AK024401 Homo sapi
16	231	49.4	2199	8	AK094005	AK094005 Homo sapi
17	186.2	39.8	744	6	BD150403	BD150403 Primer fo
18	186.2	39.8	744	6	AX870341	AX870341 Sequence

19	149.4	31.9	2625	5	BC092161	BC092161 Danio rer
20	147.8	31.6	182659	9	AC120353	AC120353 Mus muscu
21	147.8	31.6	185733	9	AC113055	AC113055 Mus muscu
22	142.6	30.5	254	10	G30716	G30716 BMS53439 Br
23	130.4	27.9	187322	14	AC122993	AC122993 Rattus no
24	130.4	27.9	220259	14	AC134763	AC134763 Rattus no
25	130.4	27.9	226877	14	AC097312	AC097312 Rattus no
26	130.4	27.9	254629	14	AC133227	AC133227 Rattus no
27	119.4	25.5	181369	8	AC146440	AC146440 Pan trogl
28	119.4	25.5	241515	14	AC147287	AC147287 Pan trogl
29	116.2	24.8	213045	14	AC093640	AC093640 Homo sapi
30	116.2	24.8	216408	14	AC092466	AC092466 Homo sapi
31	116.2	24.8	222605	8	AC010973	AC010973 Homo sapi
32	111.8	23.9	861	10	BV102674	BV102674 MARC 1563
33	93	19.9	2379	6	CQ574749	CQ574749 Sequence
34	93	19.9	2539	2	AY118801	AY118801 Drosophila
35	93	19.9	4940	6	CQ574748	CQ574748 Sequence
36	93	19.9	74697	14	AC020500	AC020500 Drosophila
37	93	19.9	153733	2	AC023681	AC023681 Drosophila
38	93	19.9	172105	2	AC104625	AC104625 Drosophila
39	93	19.9	291799	2	AB003489	AB003489 Drosophila
40	88	18.8	662	6	BD149815	BD149815 Primer fo
41	88	18.8	662	6	AX869753	AX869753 Sequence
42	73.8	15.8	225119	14	AC015894	AC015894 Homo sapi
43	67	14.3	225119	14	AC015894	AC015894 Homo sapi
44	51.8	11.1	1647	6	AR622810	AR622810 Sequence
45	51.8	11.1	21330	6	AR619814	AR619814 Sequence

ALIGNMENTS

RESULT 1	BC015301	2962 bp	mRNA	linear	ROD 25-JUL-2005
LOCUS	Mus musculus	ATP-binding cassette, sub-family B (MDR/TAP), member 8, mRNA (CDNA clone MGC:19206 IMAGE:4237894), complete cds.			
DEFINITION	BC015301	GI:15929758			
ACCESSION	BC015301.1	GI:15929758			
VERSION					
KEYWORDS	Mus musculus (house mouse)				
SOURCE					
ORGANISM	Mus musculus (house mouse)				
REFERENCE					
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedlin, T.B., Toshlyuk, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mulahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Keltman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.				
CONSRM	Mammalian Gene Collection Program Team				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
PUBMED	12477932				
REFERENCE	2 (bases 1 to 2962)				
AUTHORS	NIH MGC Project				
CONSRM	Direct Submission				
TITLE					

JOURNAL Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINTL at: <http://image.llnl.gov>
Series: IRAX Plate: 25 Row: 9 Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27753994.

FEATURES
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1. 2962

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/strain="FVB/N"
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/clone="MGC:19206 IMAGE:4237894"
/tissue_type="Kidney, normal. 5 month old male mouse."
/clone_id="NCI CGAP_Kid14"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
1. 2962
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341. 2494
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/codon_start=1
/product="ATP-binding cassette, sub-family B (MDR/TAP), member 8"
/protein_id="AAH15301.1"
/db_xref="GI:15929759"
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CDS

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YTRDHMSFVSESRKLSVQLLLLYGVGLLTFGYLVLSHIGERMAMDRLKALFSSLL
RODIAFPDAKTGQLVSRLLTGVGFSSFKLVISQGLRGTQVYISLVSLSMLSPRL
TLMIAVTPALMGVGTLMGSGRLKRSQCQEIARATGVADALGNVTRAPAFMEKR
EERYQALLESCECCABELRGIALFQGLSNIAFNCMVLTGLFISGLVAGQQLKGD
LMSFLVASQTVQSRMASLSLVFGQVVRGLSAGARVEFYMAISPIPLTGYCIPNKDI
RGSITFQNVTSYPCRPGRNVKDFTLKLPKGIKVALVVGSGGKTTVASLBERFYD
EAGSVTLGDHLRTLNPSWLRGQVGFISQEPVLFATTIMENIRFGKLDASDEEYTA
AREANAHFISFPDGYSTVGERGTTLSGGQKRLAIAPALIKOPTVLILDEATSL
DASERVVOEALDRASAGRTVLVIAHRLSTVRAHSIIVANGQVCBAGTHBELKKG
GLYSELIRQTLIDASLTSTPPAEKPEDPKSCQSKA"

ORIGIN

Query Match 88.7%; Score 415; DB 9; Length 2962;
Best Local Similarity 91.9%; Pred. No. 4.2e-94;
Matches 429; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

OY 2 ACTGAGCTGGCCTTAGTGGCGGCACTAGTGAATGTGCAGATCCCTTGCTCTGGGCCAG 61
DB 740 ATTGTGCTGGCCTTAGTGGCGGCACTAGTGAATGTGCAGATCCCTTGCTCTGGGCCAG 799
OY 62 CTGGTGAGATTGTGCGCAAGTACAGAGGACCATGGGAGTNTGNTGANTCC 121
DB 800 CTGGTGAGATTGTGCGCAAGTACAGAGGACCATGGGAGTTTCTGTCTGAGTCC 859
OY 122 CGNAAGCTCANGCNCANGTCTCTACTGACNGAGTTGAGNACTGNTGACCTTNGA 181

DB 860 CGTAAGCTCAGCGCTCCAGCTGCTCTTACTGTAAGGTGTTCAAGGACTGTGACCTTTGGA 919
OY 182 TACCTAGTGTGCTGTGTCACCATGNGANCNCATGCGCCATGACATGCGAAAGCCTT 241
DB 920 TACCTAGTGTGCTGTGTCACCATGTTGAGCGCATGCGCCATGACATGCGAAAGCCTT 979
OY 242 TTCAGTCCCTGCTCCGCGAAGACATGCTTTNTTGTATGCCAAAAAGACAGGCGAGCT 301
DB 980 TTCAGTCCCTGCTCCGCGAAGACATGCTTTCTTGTATGCCAAAAAGACAGGCGAGC-T 1038
OY 302 AGTAGTGGCTTGACTACTGATGTGCAAGAATTCAAGGCATCTTNAAGCTTGTCAATTN 361
DB 1039 AGTAGTGGCTTGACTACTGATGTGCAAGAATTCAAGGCATCTTCAAGCTTGTCAATTN 1098
OY 362 CCAGGACTGNGCAGCTGACAGCCAGGTGATTGGTAGCCTGAGNCCGTGNTATGCTGNC 421
DB 1099 CCAGGACTGCGGACAGCTGACACCAGGTGATTGGTAGCCTGCTGCTCTATGCTGTC 1158
OY 422 CCCTGCGCTTACCTGATGTGCTGCTGNNGCACACCCGCCCTCATGG 468
DB 1159 CCCTGCGCTTACCTGATGTGCTGCTGCTGTCACACCCGCCCTCATGG 1205

RESULT 2
LOCUS BC085781 2851 bp mRNA linear ROD 06-JUL-2005
DEFINITION Rattus norvegicus ATP-binding cassette, sub-family B (MDR/TAP), member 8 (predicted), mRNA (CDNA clone MGC:93731 IMAGE:7107433), complete cds.

ACCESSION BC085781
VERSION BC085781.1 GI:55715993
KEYWORDS MGC.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE
AUTHORS 1 (bases 1 to 2851)
Strausberg, R.L., Pelngold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uebdi, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McKean, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.B., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

CONSRIM
TITLE Mammalian Gene Collection Program Team
JOURNAL human and mouse cDNA sequences
PUBMED Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
REFERENCE 12477932
2 (bases 1 to 2851)

CONSRIM
TITLE NIH MGC Project
JOURNAL Direct Submission
REMARK Submitted (01-NOV-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLAST at: <http://image.llnl.gov>
 Series: IRAK Plate: 181 Row: f Column: 11
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 56119151..

FEATURES

Bouice

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/db_xref="taxon:10116"
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/clone_id="NIH_MGC_235"
/lab_host="DH10B"
/note="Vector: pExpress1"
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/gene="Abcb8_predicted"
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/db_xref="RGD:1307655"
44..2188

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CDS

genre

ORIGIN

Query Match	80.8%;	Score 378.2;	DB 9;	Length 2851;
Best Local Similarity	86.9%;	Pred. No. 8.4e-85;		
Matches 406; Conservative	0;	Mismatches 60;	Indels 1;	Gaps 1;

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 TRHEVHGSFVSESRRUSIQLLLVGVQGLTFEGLVLLSHMGSEAMDMRKALPSSLL
 RODIAFFDAKTQGLVSRLLTVDVQEFKSPFKLVISQGRSSTVOYIGSLMTLSISPR
 TMLAVVTPALMGVGLTLMGSGIRKLSRQCEOBARATGVADAEGLSVRTVAFAMKGR
 EBERRYQAELESCCCBAELGRIALFQGSIAINFNCMVLGTFPIGSLVAGQQLKGED
 LMSFLVASQTVQRSMASLSVLFGVQVRLSAGARVBYMSLSVYIPLTGYSIPSKDD
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 YAGVVTLDGHDRLTLDPSWLRQVIGFISQEBVLFATTIMENIRFGKLDASDEBYTAA
 ARKANAHFETSSFPDGSITVVGERTGLTSGQKRLAIARALIKRPTVLIDBATSA
 DAESERIVQBALDRASLSPAPPAEKPEDHRSQ"GLYAEILIRQALDASLSPAPPAEKPEDHRSQ"

Db	683	TTCA	GTCC	CTGCTC	CCGG	CAAG	ACAT	TGCTT	CTTT	GTAT	GCCA	AAAA	AGAC	AGGG	CAGC	-T	741															
Qy	302	AGT	AGT	CGCT	TGACT	ACTG	ATGT	GCA	GAAT	CA	AGG	CA	TCTT	NA	AGCT	TGT	CA	ATTN	361													
Db	742	AGT	AG	CCG	CTT	GACT	GA	TGT	GCA	GA	GTTC	CA	AGT	CA	TCTT	CA	AGCT	TGT	CA	TCTC	801											
Qy	362	CC	AGG	CA	CT	GN	AG	CT	GN	AC	CC	AG	GT	GA	TT	GT	GA	CC	CT	GG	AG	NC	CC	CT	GN	NT	AT	GT	CT	GC	NC	421
Db	802	CC	AGG	CA	CT	GC	CA	GT	CC	AC	CC	CA	AG	GT	AT	CG	GA	CC	CT	GA	TA	GA	CC	CT	GT	AT	CT	GT	CT	CT	CTC	861
Qy	422	CC	CT	GC	CT	TA	CC	CT	GA	TG	CT	GG	CT	GN	GN	NC	CA	CA	CC	CG	CC	CT	CA	TGG	468							
Db	862	CCC	GC	CC	CT	TAC	ACT	GA	TG	CT	GG	CT	GT	TT	GT	CA	CA	CA	CC	TG	CC	CT	CA	TGG	908							

RESULT 3

LOCUS	2308 bp	mRNA	linear	PRI 26-APR-2000
DEFINITION	AK222911	Homo sapiens mRNA for ATP-binding cassette, sub-family B, member 8 variant, clone: HRC04144.		

ACCESSION	AK222911	GI:62897380
VERSION	AK222911.1	
KEYWORDS	PLI_CDNA; oligo capping.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE	1
AUTHORS	Maruyama, K. and Sugano, S.
TITLE	Oligo-capping: a simple method to replace the cap structure of eukaryotic mRNAs with oligoribonucleotides
JOURNAL	Gene 138 (1-2), 171-174 (1994)
PUBMED	8125298

COMMENT

This work was supported in part by the National Project on Protein Structural and Functional Analysis, Ministry of Education, Culture, Sports, Science and Technology of Japan.

Sumio Sugano, Yutaka Suzuki
Laboratory of Functional Genomics Department of Medical Genome Sciences Graduate School of Frontier Sciences The University of Tokyo, 4-6-1 Shirokanedai, Minato-ku, Tokyo 108-8639 Japan email: asugano@k.u-tokyo.ac.jp

URL: <http://www.k.u-tokyo.ac.jp/index.html.en>.

FEATURES

Source

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source
1..2308
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/clone="HRC04144"
/cell_type="primary human renal epithelial cells"
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/evidence=not experimental
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/protein_id="BAD96631.1"
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LRQDITFFDANKTGQLVSRLLTDDVQEFKSFKLVISQGLRSTQVAGCLVLSMLSTR
LTLNVAITPALMGVGTLMGSGIRKLSRQCEQIARAMGVADBALGNVRYAFAMBO
REBRYGALEBACRCRABELGEGIALFQGLSNIAFNCVLTLPFGSLVAGQQLTG
DLMSFLVASQTVQRSMANSLVLFQGVVRLSAGARVEYMALNPCIPLSGGCCVPKEQ
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ORIGIN

Query Match 67.5%; Score 316; DB 8; Length 2308;
Best Local Similarity 78.9%; Pred. No. 4.4e-69;
Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

QY 5 GAGCTGGCCTTAGTGGCGGCACTAGTGAATGTGCAGATCCCTGCTCTGGGCGCAGCTG 64
Db 472 GTGCTGGCCTTGGTGGCGGCACTGTGAATGTACAGATCCCCCTGCTCTGGGCGCAGCTG 531
QY 65 GTGAGATTGTCCGCAAGTACACGAGGAGCACATGGGAGANTCNTGTGANTCCCGN 124
Db 532 GTAGAGGTGTGGCGCAAGTACACAGGAGCACCGTAGGAGTTTCATGACTGATGCCAG 591
QY 125 AAGCTCANGNCNCACTGCTCTACTGNACNAGATTCAAGNACTGNTGACCTTNGATAC 184
Db 592 AATCTCAGCACCCACTGCTTATCTCTATGTGTCCAGGACTGCTGACCTTCGGGTAC 651
QY 185 CTAGTGTGCTGTCCCAACATTGNNGANCATGGCCATGNACATGGGAAAGCCCTTTTC 244
Db 652 CTGGTGTGCTGTGCCACGTTGGCGAGCGCATGGCTGTGACATGGGAGGCCCTCTTC 711
QY 245 AGCTCCCTGCTCCGGCAAGACATTGCTTNTTGTATGCCAAAAAGACAGGCGAGCTAGT 304
Db 712 AGCTCCCTGCTCCGACAGACATCACCTTCTTTGACGCCAATAAGACAGGCGAGC-TGCT 770
QY 305 GAGTCGCTGACTAGTGTGCAAGAATTCAAGCATCCTTNAAGCTTGTCAATNCCA 364
Db 771 GAGCGGCTTGACAACTGACGTGACAGAGTTTAAGTCATCTTCAAGCTTGTCACTCCA 830
QY 365 GGGACTGNGACGTGNACCCAGGTGATTGTAGCCTGAGNCCCTGNNTATGTCNCCCC 424
Db 831 GGGGCTGCGAAGCTGCACCCAGGTGGAGGCTGCTGTCTCCCTGTCCATGCTGTGCAC 890
QY 425 TCGCCTTACCCTGATGCTGGCTGNNGNCAACACCCGCCCTCATGG 468
Db 891 ACGCCTCACGCTGCTGATGTGTGGCCACACAGCCCTCATGG 934

RESULT 4
AX833134 2392 bp DNA linear PAT 15-DEC-2003
LOCUS AX833134
DEFINITION Sequence 258 from Patent EP1347046.
ACCESSION AX833134
VERSION AX833134.1 GI:39919269
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Isegai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and

TITLE Masuho,Y.
JOURNAL Full-length cDNA sequences
Patent: EP 1347046-A 258 24-SEP-2003;
Research Association for Biotechnology (JP)
FEATURES
source location/Qualifiers
1. .2392
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 67.5%; Score 316; DB 6; Length 2392;
Best Local Similarity 78.9%; Pred. No. 4.4e-69;
Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

QY 5 GAGCTGGCCTTAGTGGCGGCACTAGTGAATGTGCAGATCCCTTGTCTCTGGGCGCAGCTG 64
Db 428 GTGCTGGCCTTGGTGGCGGCACTGTGAATGTACAGATCCCCCTGCTCTGGGCGCAGCTG 487
QY 65 GTGAGATTGTCCGCAAGTACACGAGGAGCACATGGGAGNTCNTGTGANTCCCGN 124
Db 488 GTAGAGGTGTGGCGCAAGTACACAGGAGCACCGTAGGAGTTTCATGACTGATGCCAG 547
QY 125 AAGCTCANGNCNCACTGCTCTACTGNACNAGATTCAAGNACTGNTGACCTTNGATAC 184
Db 548 AATCTCAGCACCCACTGCTTATCTCTATGTGTCCAGGACTGCTGACCTTCGGGTAC 607
QY 185 CTAGTGTGCTGTCCCAACATTGNNGANCATGGCCATGNACATGGGAAAGCCCTTTTC 244
Db 608 CTGGTGTGCTGTGCCACGTTGGCGAGCGCATGGCTGTGACATGGGAGGCCCTCTTC 667
QY 245 AGCTCCCTGCTCCGGCAAGACATTGCTTNTTGTATGCCAAAAAGACAGGCGAGCTAGT 304
Db 668 AGCTCCCTGCTCCGACAGACATCACCTTCTTTGACGCCAATAAGACAGGCGAGC-TGCT 726
QY 305 GAGTCGCTGACTAGTGTGCAAGAATTCAAGCATCCTTNAAGCTTGTCAATNCCA 364
Db 727 GAGCGGCTTGACAACTGACGTGACAGAGTTTAAGTCATCTTCAAGCTTGTCACTCCA 786
QY 365 GGGACTGNGACGTGNACCCAGGTGATTGTAGCCTGAGNCCCTGNNTATGTCNCCCC 424
Db 787 GGGGCTGCGAAGCTGCACCCAGGTGGAGGCTGCTGTCTCCCTGTCCATGCTGTGCAC 846
QY 425 TCGCCTTACCCTGATGCTGGCTGNNGNCAACACCCGCCCTCATGG 468
Db 847 ACGCCTCACGCTGCTGATGTGTGGCCACACAGCCCTCATGG 890

RESULT 5
AK094636 2392 bp mRNA linear PRI 30-JAN-2004
LOCUS AK094636
DEFINITION Homo sapiens cDNA FLJ37317 fis, clone BRAMY2017455, highly similar to Homo sapiens ATP-binding cassette protein M-ABCl mRNA.
ACCESSION AK094636
VERSION AK094636.1 GI:21753734
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishii,S., Yamamoto,J., Sato,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M., Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondoh,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H., Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S.,

TITLE	JOURNAL	PUBMED	REFERENCE	AUTHORS
Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imobe, N., Mutsashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Mori, Y., Momiya, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togaishi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.	human cDNAs	Complete sequencing and characterization of 21,243 full-length human cDNAs	Nat. Genet. 36 (1), 40-45 (2004)	14702039
2	Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T., Kodaira, H., Furuya, T., Takahashi, M., Kikawa, B., Omura, Y., Abe, K., Kamiyama, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.	NEBO human cDNA sequencing project	Unpublished	3 (bases 1 to 2392)
Isogai, T. and Yamamoto, J.	Direct Submission	Submitted (04-JUL-2002) Takao Isogai, FUJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan	(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)	NEBO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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		74. 2179	/note="unnamed protein product"	/codon_start=1
		/protein_id="BAC04392.1"	/db_xref="GI:21753735"	/translation="MLVHLFRVGRGGRPFGRLLPPLRQFTSAVRYSQDGRSSLLR
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		SRLLTVDQEFKSFRLVLSQGLRSCVAVGLVSLMSLSTRLLIMVATPALMGVGT	LMGSLRLKSRQCOEIVARAGVADAEALGNVTRVAFAMEQREBERYGAELRCRA	BELGRGIALFQGLSNIAFNCMVLTGLTGGSLVAGQOLTGDDMLFVLAQTVQSRMA
		NLSVLFGQVVRGLSAGARVEFMALNPCLPLSGCCVPEKQRLGSVTFQNVCSY	PGFEVLKDFTLTPPKKIVALVQSGGGKTTVASLIERFYDPTAGVAMLGDRDLRTLD	PSMLRGQVVGFIQSEPVLFQTTIMENIRFGKLEASDBEVYTAAREANAHEFTSP
		EGEG	INTVVGERTTSLGGQKRLAIARALIKOPTVLLIDELATSDALDAESERVQELADRAS	

ORIGIN	Query Match	67.5%;	Score 316;	DB 8;	length 2392;
	Best Local Similarity	78.9%;	Pred. No. 4.4e-69;		
	Matches 366;	Conservative 0;	Mismatches 97;	Indels 1;	Gaps 1;
	AGRTVLVIAHRLSTVRGAHCVVMADGRVWEAGTHEELLKKGGLYAELLRRQALDAPK TAAPPEKKKEGPRSHQHS"				
OY	5	GAGCTGGCCCTTAGGTGCGGCACTAGTAATGTGCAGATCCCTTGCTCCTGGGCCAGCTG	64		
DB	428	GTGCTGGCCCTTGGGTGCGGCACTGTAATGTACAGATCCCTTGCTCCTGGGCCAGCTG	487		
OY	65	GTGAGATTGTGCGCAAGTACACAGGGGACCATGGGGAGNTCNTGTTGANTCCCGN	124		
DB	488	GTAGAGTGTGCGCAAGTACACAGGGGACCATGGAGATTTCATGACTGATGCCAG	547		
OY	125	AAGCTCANGCNCANCTGCTCTACTGNACNGAGTTCAGNACTGNTGACCTTNGATAC	184		
DB	548	AATCTCAGCACCACTGCTTATCTCTATGTGTCCAGGACTGTGACCTTCGGGTAC	607		
OY	185	CTAGTGTGCTGTGCCACATTGNNGANCATGGCCATGNACATGGCGAAAGCCCTTTC	244		
DB	608	CTGTTGCTGTGTGCCACGTTGGCGAGCGCATGGCTGTGACATGCGAGGGCCCTTTC	667		
OY	245	AGCTCCCTGTCTCCGGAAGACATTGCTTTNTTGTATGTCGCAAAAAGACAGGGCAGCGTAGT	304		
DB	668	AGCTCCCTGTCTCCGCAAGACATCACCTTCTTGAAGCCCAATPAAGACAGGGCAGC-TGGT	726		
OY	305	GAGTGCCTTGACTACTGATGTGCAAGATTCAAGGCATCCTTNAAGCTGTCAATNCCA	364		
DB	727	GAGCGCTTGACAACTGACGTGACAGAGTTTAAGTCATCTTCAAGCTGTCACTGCCA	786		
OY	365	GGGACTGNGCAGCTGNACCCAGGTGATTGTAGCTGAGNCCCTGNTATGCTGNCCTC	424		
DB	787	GGGGCTGCGAAGCTGCACCCAGGTGCGAGCGCTGCTGTGTCCCTGTCCATGCTGTGAC	846		
OY	425	TCGCCTTACCTGATGCTGGCTGNNGCACACCCGCCCTCATGG	468		
DB	847	ACGCTCAGCGCTGCTGATGTGTGCGCACACAGCCCTGATGG	890		
RESULT 6					
LOCUS	CO717207	2417 bp	DNA	linear	PAT 03-FEB-2004
DEFINITION	Sequence 3141 from Patent WO02068579.				
ACCESSION	CO717207				
VERSION	CO717207.1	GI:42278064			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Homnidae; Homo.				
REFERENCE	1				
AUTHORS	Venter, C.J., Adams, M.C., Li, P.W. and Myers, B.W.				
TITLE	klts, such as nucleic acid arrays, comprising a majority of				
	humanexons or transcripts, for detecting expression and other uses				
	thereof				
JOURNAL	Patent: WO 02068579-A 3141 06-SEP-2002;				
FEATURES	PE Corporation (NY) (US)				
source	location/Qualifiers				
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	/organism="Homo sapiens"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
ORIGIN					
	Query Match	67.5%;	Score 316;	DB 6;	length 2417;
	Best Local Similarity	78.9%;	Pred. No. 4.4e-69;		
	Matches 366;	Conservative 0;	Mismatches 97;	Indels 1;	Gaps 1;
OY	5	GAGCTGGCCCTTAGGTGCGGCACTAGTAATGTGCAGATCCCTTGCTCCTGGGCCAGCTG	64		

Db 450 GTGCTGGCCTTGGGTGGGCACTCGTGAATGTACAGATCCCCCTGCTCTGGGCCAGCTG 509

QY 65 GTGAGATTGTGCCAAGTACACGAGGACCATGGGAGTNCNTGNTGANTCCCGN 124

Db 510 GTAGAGTGTGGCCAAAGTACACAGGAGCACGTAGGAGTTTCATGACTGATGCCAG 569

QY 125 AAGCTCANGNCANCTGCTCTACTGNACGAGTTCAAGNACTGNTGACCTTNGATAC 184

Db 570 AATCTCAGCACCACTGCTTATCTCTATGTGTGCCAGGACTGTGACCTTCGGGTAC 629

QY 185 CTAGTGTGCTGTCCACATTTGNNGANCATGGCCATGNACATGGGAAAGCCCTTTC 244

Db 630 CTGTGTGCTGTGTCCACGTTGGCGAGCGCATGGCTGTGACATGGGAGGCCCTCTTC 689

QY 245 AGCTCCCTGCTCCGGCAAGACATTGCTTTNTTGTATGCCAAAAGACAGGGCAGCTAGT 304

Db 690 AGCTCCCTGCTCCGACACAGACATCACCTTCTTTGACGCCAATAGACAGGGCAGC-TGGT 748

QY 305 GAGTCGCTGACTACTGATGTGCCAAGATTCAAGGCATCCTTNAAGCTTGTCAATNNCCA 364

Db 749 GAGCCGCTTGACAACTGACGTGCAGAGATTTAAGTCATCCTTCAAGCTTGTCACTCCCA 808

QY 365 GGGACTGNGCAGCTGNACCCAGGTGATTGTAGCCTGGAGNCCCTGNTATGTCGNCCCC 424

Db 809 GGGGCTGCGAAGCTGCACCCAGGTGCAGGCTGCTGTGTCCTGTTCATGCTGTGCAC 868

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Db 869 ACGCCTCAGCTGTGCTGATGTGTGGCCACACGACCCCTGATGG 912

RESULT 7

BD156975 2487 bp DNA linear PAT 17-JAN-2003

LOCUS BD156975

DEFINITION Primer for synthesizing full-length cDNA and use thereof.

ACCESSION BD156975

VERSION BD156975.1 GI:27862733

KEYWORDS JP 2002191363-A/11818.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2487)

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.

TITLE Primer for synthesizing full-length cDNA and use thereof

JOURNAL Patent: JP 2002191363-A 11818 09-JUL-2002;

HELEX RESEARCH INSTITUTE

COMMENT OS Homo sapiens (human)

PN JP 2002191363-A/11818

PD 09-JUL-2002

PF 28-JUL-2000 JP 2000280990

PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU

PI SAITO,

PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,

PI KEIICHI NAGAI,TETSUJI OTSUKI

PC

C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC

10,

PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC

Primer for synthesizing full-length cDNA and use thereof FH Key

Location/Qualifiers

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FEATURES

source 1..2487

Location/Qualifiers

1..2487

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 67.5%; Score 316; DB 6; Length 2487;

Best Local Similarity 78.9%; Pred. No. 4.4e-69;

Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

QY 5 GAGTGGCTTAGGTGCGGCACTAGTAATGTGCAGATCCCTTGTCTCTGGGCCAGCTG 64

Db 523 GTGTGGCTTGGGTGGGCACTCGTGAATGTACAGATCCCCCTGCTCTGGGCCAGCTG 582

QY 65 GTGAGATTGTGCCAAGTACACGAGGACCATATGGGAGTNCNTGNTGANTCCCGN 124

Db 583 GTAGAGTGTGGCCAAAGTACACAGGAGCACGTTAGGAGTTTCATGACTGATGCCAG 642

QY 125 AAGCTCANGNCANCTGCTCTACTGNACGAGTTCAAGNACTGNTGACCTTNGATAC 184

Db 643 AATCTCAGCACCACTGCTTATCTCTATGTGTCCAGGACTGTGACCTTCGGGTAC 702

QY 185 CTAGTGTGCTGTCCACATTTGNNGANCATGGCCATGNACATGGGAAAGCCCTTTC 244

Db 703 CTGTGTGCTGTGTCCACGTTGGCGAGCGCATGGCTGTGACATGGGAGGCCCTCTTC 762

QY 245 AGCTCCCTGCTCCGGCAAGACATTGCTTTNTTGTATGCCAAAAGACAGGGCAGCTAGT 304

Db 763 AGCTCCCTGCTCCGACACAGACATCACCTTCTTTGACGCCAATAGACAGGGCAGC-TGGT 821

QY 305 GAGTCGCTGACTACTGATGTGCCAAGATTCAAGGCATCCTTNAAGCTTGTCAATNNCCA 364

Db 822 GAGCCGCTTGACAACTGACGTGCAGAGATTTAAGTCATCCTTCAAGCTTGTCACTCCCA 881

QY 365 GGGACTGNGCAGCTGNACCCAGGTGATTGTAGCCTGGAGNCCCTGNTATGTCGNCCCC 424

Db 882 GGGGCTGCGAAGCTGCACCCAGGTGCAGGCTGCTGTGTCCTGTTCATGCTGTGCAC 941

QY 425 TCGCCTTACCCTGATGTGCTGNNGNACACCCGCCCTCATGG 468

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RESULT 8

AX878013 2487 bp DNA linear PAT 17-DEC-2003

LOCUS AX878013

DEFINITION Sequence 12918 from Patent EP1074617.

ACCESSION AX878013

VERSION AX878013.1 GI:40032749

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.

TITLE Primers for synthesizing full-length cDNA and their use

JOURNAL Patent: EP 1074617-A 12918 07-FEB-2001;

Research Association for Biotechnology (JP)

FEATURES

source 1..2487

Location/Qualifiers

1..2487

/organism="Homo sapiens"

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67..2274

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Query Match 67.5%; Score 316; DB 6; Length 2487;
Best Local Similarity 78.9%; Pred. No. 4.4e-69;
Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

Qy 5 GAGCTGGCCTTAGTGGCGCACTAGTAATGTGCAGATCCCTTGCTCTGGGCCAGCTG 64
Db 523 GTGCTGGCCTTGGTGGCGCACTGTAATGTACAGATCCCTTGCTCTGGGCCAGCTG 582
Qy 65 GTGGAATTGTCCGCAAGTACACGAGGACCAATGGGAGNTNCTGNTGANTCCCGN 124
Db 583 GTAGAGGTGTTGGCCAGTACACAGGAGCACGTAAGGAGTTTCATGACTGATCCCG 642
Qy 125 AAGCTCANGCNCANGCTGCTCTACTGNACNGAGTTCAGNACTGNTGACCTTNGATAC 184
Db 643 AATCTCAGACACCACCTGCTTATCCTCTATGTCGCCAGGACTGCTGACCTTCGGGTAC 702
Qy 185 CTAGTGTCTGTGTCCCACTGNNGANCATGGCCATGNACATGCGGAAGCCCTTTC 244
Db 703 CTGCTGTCTGTGTCCCACTGNNGANCATGGCCATGGCTGTGACATGCGGAGCCCTTTC 762
Qy 245 AGCTCCCTGCTCCGGCAGACATGCTTNTTGTATGCCAAAAGACAGGCGACGCTAGT 304
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Db 882 GGGGCTGCCAAGCTGCACCCAGGTGCGAGGCTGCTGTCTCCATGCTGTGCAC 941
Qy 425 TCGGCTTACCCTGATGCTGCTGNNNGACACCCCGCCTCATGG 468
Db 942 ACGCCTCAGCTGTGCTGATGTGGCCACACCGCCTGATGG 985

RESULT 9
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LOCUS Homo sapiens cDNA FLJ1156 fls, clone PLACE1006956, weakly similar
DEFINITION to ATP-DEPENDENT PERMEASE MDL1.
ACCESSION AK002018
VERSION AK002018.1 GI:7023645
KEYWORDS oligo capping; fls (full insert sequence).
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,
Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H.,
Sekine, M., Oobayashi, M., Nishi, T., Shibahara, T., Tanaka, T.,
Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y.,
Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M.,
Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H.,
Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Puruya, T.,
Kikawa, B., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K.,
Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H.,
Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M.,
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Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T.,
Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S.,
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Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T.,
Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K.,
Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M.,
Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y.,
Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N.,
Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T.,
Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K.,
Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T.,
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Sato, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K.,
Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R.,
Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.
Complete sequencing and characterization of 21,243 full-length
human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
14702039

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
2
Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,
Nishikawa, T., Nagai, K., Sugano, S., Ishibashi, T., Fujimori, K.,
Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Ishii, S., Kawai, Y.,
Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K.,
Masuho, Y. and Kanehori, K.
NEBO human cDNA sequencing project
Unpublished
3 (bases 1 to 2487)
Isogai, T. and Otsuki, T.
Direct Submission
Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEBO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.

FEATURES
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CDS
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Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,
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Sekine, M., Oobayashi, M., Nishi, T., Shibahara, T., Tanaka, T.,
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Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H.,
Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Puruya, T.,
Kikawa, B., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K.,
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ORIGIN
1
Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,
Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H.,
Sekine, M., Oobayashi, M., Nishi, T., Shibahara, T., Tanaka, T.,
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Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M.,
Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H.,
Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Puruya, T.,
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Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S.,
Yosida, M., Houta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A.,
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Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T.,
Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S.,
Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H.,

Qy 5 GAGCTGGCCTTAGTGGCGCACTAGTAATGTGCAGATCCCTTGCTCTGGGCCAGCTG 64
Db 523 GTGCTGGCCTTGGTGGCGCACTGTAATGTACAGATCCCTTGCTCTGGGCCAGCTG 582

QY	65	GTGAGATTGTGCGCAAGTACACGAGGGACCATGGGGAGTNCATGTTGANTCCCGN	124
Db	583	GTAGAGGTGTTGGCCAAAGTACACAAGGGACCACGTAGGGAGTTTCATGACTGAGTCCCGAG	642
QY	125	AAGCTCANCNCNCANCTGCTCTTA CTGNA CN GAGTT CAGNA CTGNTGACCTTNGATATAC	184
Db	643	AATCTCAGCACCCACCTGCTTA TCTCTATAGTGTCCAGGAGACTGCTGACCTTGGGTAC	702
QY	185	CTAGTGTCTGTGTCCACATTTGNNGANCNCATGGCCCATGNACATGCGGAAAGCCCTTTTC	244
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QY	305	GAGTGTCTTGACTACTGATGTGCAGAATTC AAGGCATCCTTNAAGCTTGT CATNTNCCA	364
Db	822	GAGCGGCTTGACAAC TGA CGTGCAGAGAGTTTAAGTCATCTTCAAGCTTGT CATCTCCA	881
QY	365	GGGACTGNGCAGCTGNACCCAGGTGATTG GTAGCCTGGA GNCCTGNN TATGCTGNCCCC	424
Db	882	GGGGCTGCGGAAGCTGCACCCAGGTGGCAGAGGCTGCCTGTGTCTCTGTCCATGTGTGCAC	941
QY	425	TGCGCTTACCCGTGATGTGGCTGNNGNCA CACCCGCGCCTCATGG	468
Db	942	ACGCTCTCAGCTGTGTGTGATGTGGCCACACACCA GCGCCTGATGG	985

RESULT 10			
CQ850926			
LOCUS	CQ850926	5089 bp	DNA
DEFINITION	Sequence 1395 from Patent EP1447413.	linear	PAT 23-AUG-2004

ACCESSION	CQ850926
VERSION	CQ850926.1
	GI:51509138

KEYWORDS	.
SOURCE	Homo sapiens (human)

ORGANISM Homo, sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE
AUTHORS
1
Isogai, T., Yamamoto, J., Nishikawa, T., Isono, Y., Sugiyama, T.,
Otsuki, T., Wakamatsu, A., Ishii, S., Nagai, K. and Irie, R.

TITLE	Full-length human CDNA
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JOURNAL Patent: EP 1447413-A 1395 18-AUG-2004;
Research Association for Biotechnology (JP)

FEATURES	Location/Qualifiers
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ORIGIN

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Best Local Similarity	78.9%	Pred. No. 4.5e-69;		
Matches 366;	Conservative 0;	Mismatches 97;	Indels 1;	Gaps 1;

QY 5 GAGCTGGCCTTAGGTGCGGCACCTAGTGAATGTGCAGATCCCCCTTCTCTGGGCCAGCTG 64
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 610 GTGCTGGCCTTGSGTGC GGCACTCGTGAATGTACAGATCCCCCTGCTCTGGGCCAGCTG 669

65 GTGAGATTGTCGCCAGTACACGAGGACCATGGGGAGNTNCTGTNTGANTCCCGN 124

Db 670 GTAGAGTCTGSCCACTACACAGAAGCACTAGGAGTTTCATGACTGAGTCCAG 729

125 AAGTCANCGNCANCTGCTCCTACTGNA¹NGAGTTCAGGNACTGNTGACCTTNGGATAC 184

Db 730 AATCTAGCACCCACTGTTATCTCTATGTGTCCAGGACTGTGACCTTCCGGTAC 789

QY 185 CTAGTGTCTGTCCTCCACATTGANGANCATGGCCATGNACATGGGAAGCCCTTTTC 244

Db	790	CTGTGCTGCTGTGTCCACGTTGGCGAGCGCATGGCTGTGACATGCGAGGGGCGCTCTTC	849
QY	245	AGCTCCCTGCTCCGGGAGAACAATTGCTTNTTGTATGCCAAAAAGACAGGGGACGCGTAGT	304
Db	850	AGCTCCCTGCTCCGACACAGACATCACCTTCTTTGACGCCCAATTAAGACAGGGGACGC-TGGT	908
QY	305	GAGTCGCTTGACTACTGATGTGTGCAAGAATTCAAGGCATCCTTNAAGCTGTGCATNTNCCA	364
Db	909	GAGCCGCTTGGACAACCTGACGTGACGAGAGTTTAAGTCATCTCTTCAAGCTGTGCATCTCCCA	968
QY	365	GGGACTGNGCAGCTGNAACCCAGGTGATTGGTAGCGCTGGAAGNCCCTGNTATGCTGNCCCC	424
Db	969	GGGGCTGCAGAGCTGCACCCAGGTGGCAGGCTGCTGTGTCTCCCTGTCCATGTCTGTGCAC	1028
QY	425	TCGCCTTACCCCTGATGTGCTGGCTGNNGNCAACCCCGCCCTCATGG	468
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RESULT 11
AK128129

LOCUS	AK128129	5089 bp	mRNA	linear	PRI 19-FEB-2004
DEFINITION	Homo sapiens cDNA FLJ46250 fis, clone T8ST14021569, moderately similar to ATP-binding cassette, sub-family B, member 8, mitochondrial precursor.				

ACCESSION AK128129
VERSION AK128129.1 GI:34535347
KEYWORDS oligo capping; fls (full insert sequence).

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS

TITLE
Sugliyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K., Masuno, Y., Nagai, K. and Isogai, T.
NEBO human cDNA sequencing project

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 5089)
AUTHORS Isogai, T. and Yamamoto

TITLE	Direct Submission	T
JOURNAL	Submitted (15-JUL-2003)	

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail: genomic@nri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
COMMENT

Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: Reverse Proteomics Research Institute, HRI and RAB.

FEATURES

Location/Qualifiers

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REFERENCE 1 (bases 1 to 2383)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002191363-A 15507 09-JUL-2002;
HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002191363-A/15507
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
PI SAITO,
PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
PI KEIICHI NAGAI,TETSUJI OTSUKI
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
10', C12P21/02,C12Q1/68//C12P21/08 G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
FT CDS (524) . . (2167) .
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Source Location/Qualifiers
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Query Match 64.6%; Score 302.4; DB 6; Length 2383;
Best Local Similarity 78.4%; Pred. No. 1.2e-65;
Matches 364; Conservative 0; Mismatches 98; Indels 2; Gaps 2;

QY 5 GAGCTGGCCTTAGGTGCGGCACTAGTGAATGTCAGATCCCTTGCTCTGGGCCAGCTG 64
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Db 838 ACGCCTCACGCTGCTGATGTGGCCACACGACCCCTGATGG 881
RESULT 14
AX884014 2383 bp DNA linear PAT 17-DEC-2003
LOCUS AX884014
DEFINITION Sequence 18919 from Patent EP1074617.
ACCESSION AX884014
VERSION AX884014.1 GI:40038915
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primers for synthesizing full-length cDNA and their use
JOURNAL Patent: BP 1074617-A 18919 07-FEB-2001;
Research Association for Biotechnology (JP)
FEATURES
Source Location/Qualifiers
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CDS
ORIGIN
Query Match 64.6%; Score 302.4; DB 6; Length 2383;
Best Local Similarity 78.4%; Pred. No. 1.2e-65;
Matches 364; Conservative 0; Mismatches 98; Indels 2; Gaps 2;

QY 5 GAGCTGGCCTTAGGTGCGGCACTAGTGAATGTGACATCCCTTGCTCTGGGCCAGCTG 64
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QY 365 GGGACTGNGCAGCTGNACCCAGGTGATTGGTAGCCTGGAGNCCCTGNTATGCTGNCCCC 424
Db 778 GGGGCTGCGAAGCTGACCCAGGTGCGAGGCTGCTGTGTCCCTGTCCATGCTGTGCAC 837
QY 425 TCGCCTTACCCTGATGTGCTGNNGNCACACCGCCCTCATGG 468
Db 838 ACGCCTCACGCTGCTGATGTGGCCACACGACCCCTGATGG 881
RESULT 15
AK024401 2383 bp mRNA linear PRI 30-JAN-2004
LOCUS AK024401
DEFINITION Homo sapiens cDNA FLJ14339 fis, clone SKNC1000013, highly similar

to Homo sapiens ATP-binding cassette protein M-ABCl mRNA, nuclear gene encoding mitochondrial protein.

ACCESSION AK024401
VERSION AK024401.1 GI:10436780
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS

1 Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Makamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuma, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hirao, K., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togaashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs

JOURNAL Nat. Genet. 36 (1), 40-45 (2004)
PUBMED 14702039

REFERENCE
AUTHORS

2 Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sato, H., Sugano, S., Shiratori, A., Sudo, H., Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T. NEDO human cDNA sequencing project

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

3 (bases 1 to 2383)
Isogai, T. and Otsuki, T.
Direct Submission
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

FEATURES
SOURCE

Location/Qualifiers
1..2383
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SKNMC1000013"

/cell_line="SK-N-MC"
/cell_type="neuroepithelioma"
/clone_lib="SKNMC1"
/note="cloning vector: pME18SFL3"
misc_difference 479^480
/note="compared to AF047690 and AC010973.4"
/replace="g"

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Best Local Similarity 78.4%; Pred. No. 1.2e-65;
Matches 364; Conservative 0; Mismatches 98; Indels 2; Gaps 2;
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Db 420 GTGCTGGCTTGGGTGGCGCACTCGTGAATGTACAGATCCCTGCTCTGGCCAGCT- 478
QY 65 GTGAGATTGTCCGCAAGTACACGAGGACCAATGGGAGNTGNTGANTCCCGN 124
Db 479 GTAGAGTGTGTGGCCAGTACACAGGACCAAGTGGAGTTCACTGAGTCCAG 538
QY 125 AAGCTCAGCAGCAGTCT 184
Db 539 AATCTCAGCAGTCT 598
QY 185 CTAGTCTGCTGTCCCAATTTGNNGNCATGGCCATGACATGCGAAGCCCTTTTC 244
Db 599 CTGCTGCTGTGTCCCAATTTGNNGNCATGGCCATGACATGCGAAGCCCTTTTC 658
QY 245 AGCTCCCTGCTCCGCAAGACATTTGTTTGTATGCCAAAAGACAGGCGAGCTAGT 304
Db 659 AGCTCCCTGCTCCGCAAGACATTTGTTTGTATGCCAAAAGACAGGCGAGCTAGT 717
QY 305 GAGTCCCTGCTAGTATGTGCAAGATTCAGGCATCCTTNAAGCTTGTCAATNTNCA 364
Db 718 GAGCTCCCTGCTAGTATGTGCAAGATTCAGGCATCCTTNAAGCTTGTCAATNTNCA 777
QY 365 GGGACTGNGCAGCTGNAACCGAGTATGTTGTTAGCTTGAAGNCCCTGNTATGCTGNC 424
Db 778 GGGCTGCGAAGCTGCAACCGAGTATGTTGTTAGCTTGAAGNCCCTGNTATGCTGNC 837
QY 425 TCGCTTACCTGATGTGCTGNNGNCACACCGCCCTCATGG 468
Db 838 ACGCTCAGCTGCTGATGTGTCACACCGCCCTCATGG 881

Search completed: January 20, 2006, 21:31:17
Job time : 3024 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: January 20, 2006, 16:27:08 ; Search time 470 Seconds
(without alignments)
6636.332 Million cell updates/sec

Title: US-10-327-713-267
Perfect score: 468
Sequence: 1 gactgagctggccttagtgg.....ngncacaccgcctcatgg 468

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3:	geneseqn2000s:*
4:	geneseqn2001as:*
5:	geneseqn2001bs:*
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8:	geneseqn2003as:*
9:	geneseqn2003bs:*
10:	geneseqn2003cs:*
11:	geneseqn2003ds:*
12:	geneseqn2004as:*
13:	geneseqn2004bs:*
14:	geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	316	67.5	2392	11	ADM01573	Adm01573 Human CDN
2	316	67.5	2417	6	ABK34832	Abk34832 Human CDN
3	316	67.5	2487	4	AAH14983	Aah14983 Human CDN
4	316	67.5	2562	3	AAD00603	Aad00603 Human mem
5	316	67.5	3212	13	ACN41862	Acn41862 Human dia
6	316	67.5	5089	13	ADR07889	Adr07889 Full leng
7	315	67.3	1211	3	AAC76613	Aac76613 Human ORF
8	302.4	64.6	2383	4	AAH18672	Aah18672 Human CDN
9	277.6	59.3	1251	3	AAA62022	Aaa62022 Hydrophob
10	277.6	59.3	1617	3	AAA62032	Aaa62032 Hydrophob
11	230	49.1	2317	13	ACN41861	Acn41861 Human dia
12	219.6	46.9	1805	6	ABL89954	Ab189954 Human pol
13	206.8	44.2	494	9	ACH43729	Ach43729 Human foe
14	206.8	44.2	1023	3	AAF22411	Aaf22411 Human sec
15	186.2	39.8	744	4	AAH08411	Aah08411 Human CDN
16	127.8	27.3	423	4	AAF92351	Aaf92351 Bovine ma
17	117.6	25.1	425	9	ACH47047	Ach47047 Human inf
18	93	19.9	2379	4	ABL03511	Ab103511 Drosoph11
19	93	19.9	4940	4	ABL03510	Ab103510 Drosoph11

20	88	18.8	662	4	AAH07823	Aah07823 Human CDN
21	74	15.8	283	4	AAL02675	Aal02675 Human rep
c 22	74	15.8	283	5	AAS40273	Aas40273 DNA encod
c 23	74	15.8	283	11	ADJ09268	Adj09268 Human pro
24	55.4	11.8	574	6	ABL90156	Ab190156 Human pol
25	51.8	11.1	1647	14	ACL67748	Ac167748 M. xanthu
26	51.8	11.1	1773	13	ADT44704	Adt44704 Bacterial
27	51.8	11.1	21330	14	ACL64746	Ac164746 M. xanthu
c 28	46.4	9.9	560	3	AAC76564	Aac76564 Human ORF
29	46.4	9.9	1743	14	ACL67610	Ac167610 M. xanthu
30	46.4	9.9	1773	13	ADT44685	Adt44685 Bacterial
31	46.4	9.9	24602	14	ACL64739	Ac164739 M. xanthu
32	44	9.4	434	5	ABV30083	Abv30083 Human pro
33	44	9.4	483	5	ABV45565	Abv45565 Human pro
34	40.8	8.7	9104	13	ADQ39136	Adq39136 Human SNP
35	40.8	8.7	9258	12	ADP45448	Adf45448 Human vas
36	40.8	8.7	9260	12	ADQ87183	Adq87183 Human tum
37	40.8	8.7	9260	12	ADQ84906	Adq84906 Human tum
38	40.8	8.7	9272	8	ABX76157	Abx76157 Lung canc
39	40.8	8.7	9272	12	ADQ18965	Adq18965 Human sof
40	40.8	8.7	9272	13	ADU05813	Adu05813 Novel bro
41	40.8	8.7	9272	14	ADX05806	Adx05806 Cyclin-de
42	40.8	8.7	9277	13	ADQ39138	Adq39138 Human SNP
43	40.8	8.7	9287	6	ABK64501	Abk64501 Human ben
44	40.8	8.7	9456	12	ADQ23327	Adq23327 Human sof
45	40.2	8.6	455	9	ACH12996	Ach12996 Human adu

ALIGNMENTS

RESULT 1	
ADM01573	ADM01573 standard; cDNA; 2392 BP.
ID	ADM01573;
XX	AC ADM01573;
XX	AC
XX	20-MAY-2004 (first entry)
DT	
XX	Human cDNA of the invention SEQ ID NO:258.
DE	
XX	
KW	ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.
XX	
OS	Homo sapiens.
XX	
PN	EP1347046-A1.
XX	
PD	24-SEP-2003.
XX	
PP	12-APR-2002; 2002EP-00008400.
XX	
PR	22-MAR-2002; 2002JP-00137785.
XX	
PA	(REAS-) RES ASSOC BIOTECHNOLOGY.
XX	
PI	Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S, Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I; Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
PI	
XX	WPI; 2003-723558/69.
DR	P-PSDB; ADM04016.
XX	
PT	New polynucleotides and polypeptides are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.
PT	
XX	
PS	Claim 1; SEQ ID NO 258; 305pp; English.
XX	
CC	The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC	

CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC cDNA sequence of the invention.

XX
SQ Sequence 2392 BP; 413 A; 766 C; 747 G; 466 T; 0 U; 0 Other;

Query Match 67.5%; Score 316; DB 11; Length 2392;
Best Local Similarity 78.9%; Pred. No. 9.9e-81;
Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

QY 5 GAGCTGGCCTTAGGTGCGGCACTAGTAATGTGAGATCCCTTGCTCCTGGCCAGCTG 64
DB 428 GTGCTGGCCTTGGGTGGGCACTGTGAATGTACAGATCCCCCTGCTCTGGCCAGCTG 487
QY 65 GTGAGATTGTGCGCAAGTACACGAGGACCATGCGAGTNCNTGNTGANTCCCGN 124
DB 488 GTAGAGGTGTTGGCCAAAGTACACAAGGGACCATGAGAGTTTCACTGAGTCCAG 547
QY 125 AAGCTCANGNCANCTGCTCTACTGNACNGAGTTCAGNACTGNTGACCTTNGATAC 184
DB 548 AATCTACAGACCCACCTGCTTATCCTATGTGTGCCAGACTGTGACCTTCGGGTAC 607
QY 185 CTAGTGTGCTGTCCCAATGNNGANCATGCGCATGNACATGCGGAAAGCCCTTTC 244
DB 608 CTGCTGTGCTGTGCCAGTTGGCGAGCGCATGCTGTGACATGGGAGGCCCTCTTC 667
QY 245 AGCTCCCTGCTCCGGAAGACATTGCTTTNTTGTATGCCAAAAGACAGGGCAGCTAGT 304
DB 668 AGTCCCTGCTCCGACAGACATCACCCTCTTTGACGCCAATAAGACAGGGCAGC-TGGT 726
QY 305 GAGTCGCTTGACTACTGATGTGCAAGAATTCAAGGACATCCTTNAAGCTTGTCAATNCCA 364
DB 727 GAGCCGCTTGACAACCTGACGTGACGAGAGTTTAAGTCAITCCTTCAAGCTTGTCACTCCA 786
QY 365 GGGACTGNGCAGCTGNACCCAGGTGATTGTGAGCTGAGNCCCTGNNATATGTCNCCC 424
DB 787 GGGGCTGCGAAGCTGACCCAGGTGGCAGGCTGCTGTGTCCTGTCCATGCTGTGAC 846
QY 425 TCGCCTTACCTGATGCTGCTGNNGNACACCGCCCTCATGG 468
DB 847 ACGCTCACGCTGCTGTGATGTGTGCCACACCAAGCCCTGATGG 890

RESULT 2
ABK34832
ID ABK34832 standard; cDNA; 2417 BP.

XX AC ABK34832;
XX DT 08-MAY-2002 (first entry)
XX DE Human cDNA for novel secreted protein, SEQ ID 601.

XX
KW Human; ss; gene; secreted protein; immune deficiency; viral infection;
KW bacterial infection; fungal infection; autoimmune disorder; burn;
KW rheumatoid arthritis; multiple sclerosis; autoimmune thyroiditis;
KW diabetes; allergy; asthma; neurodegenerative disease; Crohn's disease;
KW Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour;
KW coagulation disorder; haemophilia; inflammatory disorder; ulcer;
KW tissue regeneration; wound healing; haematopoiesis; myeloid deficiency;
KW lymphoid cell deficiency.

XX OS Homo sapiens.
XX PN WO200177290-A2.
XX PD 18-OCT-2001.
XX PF 29-MAR-2001; 2001WO-US010295.
XX PR 06-APR-2000; 2000US-0194941P.

XX
PA (GENY) GENETICS INST INC.
XX
PI Wong GG, Clark HF, Fectel K, Agostino MJ, Howes SH, Resnick RJ,
PI Gulukota K, Graham JR;
XX
DR WPI; 2002-179323/23.

XX
XX
PT Six hundred and twenty five polynucleotides derived from a variety of
PT human tissue sources which encode secreted proteins, useful for treating
PT immune deficiencies and disorders such as autoimmune disorders.

PS Claim 1; Page 324; 339pp; English.

XX
XX
CC The invention relates to 625 polynucleotides which have been derived from
CC a variety of human tissue sources and which encode novel secreted
CC proteins, their complements and sequences that hybridise to them. Also
CC included are a vector comprising the polynucleotide, a host cell
CC transformed with the vector, the proteins encoded by the polynucleotides,
CC antibodies that bind to the proteins and identification of modulators of
CC the proteins or the expression of the polynucleotide. The polynucleotides
CC can be used as probes for the identification and isolation of full length
CC cDNA and genomic DNA. The polynucleotides and proteins can also be used
CC as nutritional supplements. The protein is useful in the treatment of
CC various immune deficiencies and disorders such as viral infections,
CC bacterial infections, fungal infections, autoimmune disorders (e.g.
CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and
CC diabetes) and allergic reactions and conditions (e.g. asthma). They are
CC also useful for treating neurodegenerative diseases (e.g. Alzheimer's
CC disease, Parkinson's disease), liver fibrosis, coagulation disorders
CC (e.g. haemophilia), inflammatory disorders (e.g. Crohn's disease) and
CC tumours. They are also useful for tissue regeneration, for wound healing
CC and in the treatment of burns, incisions and ulcers. The proteins are
CC also useful for regulating haematopoiesis, for treating myeloid or
CC lymphoid cell deficiencies. The present sequence is one of the 625 cDNA
CC sequences encoding a secreted protein

XX
SQ Sequence 2417 BP; 411 A; 776 C; 755 G; 475 T; 0 U; 0 Other;

Query Match 67.5%; Score 316; DB 6; Length 2417;
Best Local Similarity 78.9%; Pred. No. 9.9e-81;
Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

QY 5 GAGCTGGCCTTAGGTGCGGCACTAGTAATGTGAGATCCCTTGCTCCTGGCCAGCTG 64
DB 453 GTGCTGGCCTTGGGTGGGCACTGTGAATGTACAGATCCCCCTGCTCTGGGCCAGCTG 512
QY 65 GTGAGATTGTGCGCAAGTACACGAGGACCATGCGGAGTNCNTGNTGANTCCCGN 124
DB 513 GTAGAGGTGTTGGCCAAAGTACACAAGGACCATGAGGAGTTTCATGACTGATGCCAG 572
QY 125 AAGCTCANGNCANCTGCTCTACTGNACNGAGTTCAGNACTGNTGACCTTNGATAC 184
DB 573 AATCTACAGACCCACCTGCTTATCCTATGTGTGCCAGGACTGTGACCTTCGGGTAC 632
QY 185 CTAGTGTGCTGTCCCAATGNNGANCATGCGCATGNACATGCGGAAAGCCCTTTC 244
DB 633 CTGCTGTGCTGTCCACGTTGGCGAGCGCATGCTGTGACATGGGAGGCCCTCTTC 692
QY 245 AGCTCCCTGCTCCGGAAGACATTGCTTTNTTGTATGCCAAAAGACAGGGCAGCTAGT 304
DB 693 AGCTCCCTGCTCCGAACAAGACATCCTTCTTGAAGCCCAATGAACAGGGCAGC-TGGT 751
QY 305 GAGTCGCTGACTACTGATGTGCAAGAATTCAAGGCATCCTTNAAGCTTGTCAATNCCA 364
DB 752 GAGCCGCTTGACAACCTGACGTGACGAGATTAAATCATCTTCAAGCTTGTCACTCCA 811
QY 365 GGGACTGNGCAGCTGNACCCAGGTGATTGTGAGCTGAGNCCCTGNNATATGTCNCCC 424
DB 812 GGGGCTGCGAAGCTGACCCAGGTGCGAGGCTGCTGTGTCCTGTCCATGCTGTGAC 871
QY 425 TCGCCTTACCTGATGCTGCTGNNGNACACCGCCCTCATGG 468

Db 872 ACGCCTCAGCTGCTGTGATGTGGCCACACGCCCTGATGG 915

RESULT 3
AAH14983
ID AAH14983 standard; cDNA; 2487 BP.

XX AC AAH14983;
XX DT 26-JUN-2001 (first entry)

XX Human cDNA sequence SEQ ID NO:12918.
DE Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX Homo sapiens.
XX EP1074617-A2.
XX 07-FEB-2001.
XX 28-JUL-2000; 2000EP-00116126.
XX 29-JUL-1999; 99JP-00248036.
XX 27-AUG-1999; 99JP-00300253.
XX 11-JAN-2000; 2000JP-00118776.
XX 02-MAY-2000; 2000JP-00183767.
XX 09-JUN-2000; 2000JP-00241899.
XX (HELI-) HELIX RES INST.
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
XX Claim 8; SEQ ID NO 12918; 2537bp + Sequence Listing; English.
XX The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
SQ Sequence 2487 BP; 440 A; 788 C; 777 G; 482 T; 0 U; 0 Other;

Query Match 67.5%; Score 316; DB 4; Length 2487;
Best Local Similarity 78.9%; Pred. No. 1e-80;
Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

OY 5 GAGCTGGCCTTAGGTGCGGCACTAGTAATGTGCAGATCCCTTGCTCCTGGGCCAGCTG 64

Db 523 GTGCTGGCCTTAGGTGCGGCACTCGTGAATGTACAGATCCCCCTGCTGGGCCAGCTG 582

OY 65 GTGAGATTGTGCGCAAGTACACGAGGACCAATGCGGAGNTNCTNTGANTCCCGN 124
Db 583 GTAGAGTGTGCGCAAGTACACAGGAGCACTAGGAGTTTCACTGAGTCCAG 642

OY 125 AAGCTCANCNCANCTGCTCCTACTGNAAGTTCAAGNACTGNTGACCTTNGATAC 184
Db 643 AATCTCAGACCCACCTGCTTATCCTTATGTGTGCCAGGACTGCTGACCTTCGGGTAC 702

OY 185 CTAGTCTGCTGTCCCAATTTGNNGANCATGGCCATGNACATGCGGAAAGCCCTTTTC 244
Db 703 CTGCTGCTGTGTCCCAAGTTGGCGAGCGCATGGCTGTGACATGCGGAGGCCCTTTC 762

OY 245 AGCTCCCTGCTCCGCGAAGACATTTGCTTTTGTATGCCAAAAGACAGGCGAGTAGT 304
Db 763 AGCTCCCTGCTCCGACAGACATCATCTTTTGAACGCCAATTAAGACAGGCGAGC-TGGT 821

OY 305 GAGTCGCTTGACTAGTATGTGCAGAATTCAAGGCATCCTTNAAGCTTGTCAATNTCCA 364
Db 822 GAGCCGCTTGACAACTGACGTGCAGAGATTAACTCATCTTCAAGCTTGTCACTCCCA 881

OY 365 GGGACTGNGCAGCTGNACCCAGTGATTTGTAAGCTGAGNCCCTGNNTATGTCGNCCCC 424
Db 882 GGGGCTGCGAAGCTGCACCCAGGTGGCAGGCTGCTGTGTCCTGTTCATGTCTGCAC 941

OY 425 TCGCCTTACCCTGATGTGCTGNNGNCAACCGCCCTCATGG 468
Db 942 ACGCCTCAGCTGCTGTGATGTGTGGCCACACGACCCCTGATGG 985

RESULT 4
AAD00603
ID AAD00603 standard; cDNA; 2562 BP.

XX AAD00603;
XX 29-AUG-2000 (first entry)

XX Human membrane transport protein, MTRP-4 cDNA.
XX Human; membrane transport protein; MTRP-4; antiinflammatory; cyostatic;
KW antithyroid; immunosuppressive; chryomimetic; antidiabetic; nootropic;
KW antidiarrhetic; neuroprotective; antidepressant; nephrotropic; virucide;
KW antihelminthic; protozoacide; antibacterial; neuroleptic; antigout;
KW diagnosis; prevention; treatment; membrane transport disorder; epilepsy;
KW Menkes disease; diabetes; Parkinson's disease; neurological disorder;
KW Alzheimer's disease; depression; schizophrenia; immune disorder; allergy;
KW inflammatory disorder; AIDS; Addison's disease; atherosclerosis; gout;
KW Graves disease; Hashimoto's thyroiditis; microbial infection; cancer;
KW cell proliferative disorder; ss.
XX
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 79..2235
FT /*tag= a
FT /product= "Membrane transport protein-4"

XX WO200026245-A2.
XX 11-MAY-2000.
XX PD
XX 04-NOV-1999; 99WO-US026048.
XX PF
XX 04-NOV-1998; 98US-0172255P.
XX PR 24-NOV-1998; 98US-0172252P.
XX PR 22-DEC-1998; 98US-0172214P.
XX PR 26-FEB-1999; 99US-0121896P.
XX (INCY-) INCYTE PHARM INC.
XX

PI Hillman JL, Yue H, Tang YT, Lai P, Corley NC, Guegler KJ;
PI Baughn MR, Azimzai Y, Lu DAM;
XX WPI; 2000-365576/31.
DR P-PSDB; AAY71059.
XX
PT Novel human membrane transport proteins useful for diagnosis, prevention
PT and treatment of membrane transport disorders, immune/inflammatory
PT disorders and cell proliferative disorders including cancer.
XX
PS Claim 9; Page 113-114; 136pp; English.
XX
CC The present sequence is a cDNA encoding membrane transport protein, MTRP-
CC 4 from Incyte clone 2274290 isolated from human PROSNON01 cDNA library.
CC MTRP-4 shows homology to human ATP-binding cassette (ABC) transporter (GI
CC 4321407) and Schistosoma mansoni ABC family protein, SMDR1. It is
CC expressed in reproductive, nervous, gastrointestinal and
CC haematopoietic/immune tissues. The present sequence is useful in
CC diagnosis, prevention and treatment of disorders related with increased
CC or decreased expression of MTRP such as familial goitre, Menkes disease,
CC diabetes, Parkinson's disease, neurological disorders such as Alzheimer's
CC disease, depression, epilepsy, schizophrenia, immune/inflammatory
CC disorders such as AIDS, Addison's disease, allergies, atherosclerosis,
CC Graves disease, gout, Hashimoto's thyroiditis, viral, bacterial, fungal,
CC parasitic, protozoal or helminthic infections and cell proliferative
CC disorders such as cancer. Fragments of MTRP polynucleotides are useful as
CC targets in microarrays. MTRP DNA is also useful for generating
CC hybridisation probes useful in mapping genomic sequences and detecting
CC differences in sequences among normal, carrier and affected individuals.
CC It is also used for screening libraries of compounds in drug screening
CC techniques
XX
SQ Sequence 2562 BP; 444 A; 824 C; 793 G; 501 T; 0 U; 0 Other;

Query Match 67.5%; Score 316; DB 3; Length 2562;
Best Local Similarity 78.9%; Pred. No. 1e-80;
Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;
QY 5 GAGCTGGCCTTAGTGGCGGCACTAGTGAATGTCAGATCCCTTGCTCTGGGCCAGCTG 64
DB 484 GTGCTGGCCTTGCGGTGGGCACTCGTGAATGTACAGATCCCCCTGCTCTGGGCCAGCTG 543
QY 65 GTGAGATTGTGCGCAAGTACACGAGGAGCAATGGGAGANTGNTGANTCCCGN 124
DB 544 GTAGAGGTGCTGGCCAAATACACAGGAGCACGTAAGGAGTTTCATGACTGATCCCAAG 603
QY 125 AAGCTCANCGNCCACTGCTCTACTGACNAGATTCAAGNACTGATGACCTTNGATAC 184
DB 604 AATCTCAGACACCACCTGCTTATCTCTATGTGTGTCCAGGACTGCTGACCTTCGGGTAC 663
QY 185 CTAGTGTGCTGTCCCATGTCATGNNGANCATGCGCATGNACATGCGGAAAGCCCTTTC 244
DB 664 CTGGTGTGCTGTCTCCACGTTGGCGAGCGCATGCTGTGACATGCGAGGGCCCTTTC 723
QY 245 AGCTCCCTGCTCCGGCAGACATTGCTTTTNTGATGCCAAAAAGACAGGGCAGCGTAGT 304
DB 724 AGCTCCCTGCTCCGACAGACATCACTTCTTGAACGCCAATAAGACAGGGCAGC-TGGT 782
QY 305 GAGTCCTTGACTACTGATGTGCAAGAATTCAGGCATCCTTNAAGCTTGTCAATNTNCA 364
DB 783 GAGCCGCTTGACACTGACGTGACGAGAGTTTAAGTCATCCTTCAAGCTTGTCACTCCA 842
QY 365 GGGACTGNGCAGCTGNACCCAGGTGATTGTAGCTTGAGNCCCTGNNATAGCTGNCCCC 424
DB 843 GGGGCTGCGAAGCTGCACCCAGGTGGCAGGGCTGCTGTGCTCCCTGTTCATGCTGCAC 902
QY 425 TCGCCTTAACCTGATGCTGGCTGNNNGACACACCCGCTCATGG 468
DB 903 ACGCCTCAGCCTGCTGTGATGTGTGGCCACACCAAGCCCTGATGG 946

RESULT 5
ACN41862

ID ACN41862 standard; cDNA; 3212 BP.
XX
AC ACN41862;
XX
DT 18-NOV-2004 (first entry)
XX
DB Human diagnostic and therapeutic polynucleotide SEQ ID NO:737.
XX
KM ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;
KM dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Hartschorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstl EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RB, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kilton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
XX WPI; 2004-329368/30.
DR P-PSDB; ABM83210.
DR
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 1; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germ-line
CC gene therapy. The present sequence represents a dithp polynucleotide of
CC the invention. Note: The sequence data for this patent is not represented
CC in the printed specification, but was obtained in electronic format
CC directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 3212 BP; 565 A; 1056 C; 938 G; 653 T; 0 U; 0 Other;

Query Match 67.5%; Score 316; DB 13; Length 3212;
Best Local Similarity 78.9%; Pred. No. 1.1e-80;
Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;
QY 5 GAGCTGGCCTTAGTGGCGGCACTAGTGAATGTGAGATCCCTTGCTCTGGGCCAGCTG 64
DB 538 GTGCTGGCCTTGCGGTGGGCACTCGTGAATGTACAGATCCCTTGCTCTGGGCCAGCTG 597
QY 65 GTGAGATTGTGCGCAAGTACACGAGGAGCACATGGGAGANTGNTGANTCCCGN 124
DB 598 GTAGAGGTGCTGGCCAAAGTACACAGGAGCACAGTAGGAGATTTCATGACTGAGTCCCAAG 657

QY	125	AAAGTCANCGNCCANCTGCTCTTA	CTAGTACN	AGAGTT	CAGGNA	CTGNTGA	CACTTNG	ATAC	184
Db	658	AATCTCAGCACCCACCTGCTTAT	CTCTAT	GTGTG	TCAGGGA	CTGTGA	CACTTC	GGGTAC	717
QY	185	CTAGTGTGCTGTCTCCACAT	TGNNG	ANCNC	ATGCGC	CATGN	ACATG	CGGAAAGCCCTTTTC	244
Db	718	CTGTGTCTGTCTGCCACG	TTGGCG	AGCGCAT	GTGGTGT	GACATG	CGGAGG	CCCTCTTC	777
QY	245	AGCTCCCTGCTCCGGA	GACATG	CTTTNT	TGATG	CCAAA	AGACAG	GGCAGCGTAGT	304
Db	778	AGCTCCCTGCTCCGCA	CAAGAC	ATCACT	TTTGAC	CGCAAT	AGACAG	GGCAGC-TG	836
QY	305	GAGTCGCTTGACTACT	GTGATG	TGCA	AGAA	TTCAAG	GCATCCTT	NAAGCTTGTCAT	NTNCCA 364
Db	837	GAGCCGCTTGACAA	CTGACGTG	CAGAGTT	TAAGTCA	TCTTCA	AGCTTGTCAT	CTCCCA	896
QY	365	GGGACTGNGCAGCTG	NACCCAG	GTGAT	TGTA	GCCTG	GAGNCCCTG	NNATATGCTG	NCCCC 424
Db	897	GGGGCTGCGAAGCT	GCACCCAG	TGCGAG	GGCTG	CTGTG	TCTTCCCTG	TCCATGCTG	TCGAC 956
QY	425	TGCGCTTACCCCTG	ATGCTG	GCTG	TGNNG	NCA	CACCCG	CCCTCAT	TGG 468
Db	957	ACGCTCA	CGCTG	CTGCTG	TGATG	TGTG	GCACAC	CAAGCCCTG	ATGG 1000
RESULT 6									
ID	ADR07889	standard; cDNA; 5089 BP.							
XX	ADR07889;								
DT	04-NOV-2004	(first entry)							
DE	Full length human cDNA useful for treating neurological disease Seq 1395.								
XX	gene; ss; human; oligo-capping method; diagnostic marker; gene therapy;								
KW	osteoporosis; neurological disease; Alzheimer's disease;								
KW	Parkinson's disease; dementia; short memory; cancer;								
KW	sense or motor function; emotional reaction; fear response; panic;								
KW	osteopathic; neuroprotective; nootropic; antiparkinsonian; cyostatic;								
KW	tranquilliser.								
XX	Homo sapiens.								
OS									
XX	BP1447413-A2.								
PN									
XX	18-AUG-2004.								
PD									
XX	12-FEB-2004; 2004EP-00003145.								
PF									
XX	14-FEB-2003; 2003JP-00102207.								
PR	09-MAY-2003; 2003JP-00131452.								
PR									
XX	(REAS-) RBS ASSOC BIOTECHNOLOGY.								
PA									
XX	Ibogaï T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;								
PI	Wakamatsu A, Ishii S, Nagai K, Irie R;								
XX									
DR	WPI; 2004-583265/57.								
DR	P-PSDB; ADR09845.								
XX									
PT	New 1995 cDNA, useful for treating osteoporosis, neurological diseases,								
PT	Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.								
XX									
PS	Claim 1; SEQ ID NO 1395; 2686bp; English.								
XX									
CC	This invention relates to novel, isolated full length human cDNA								
CC	molecules and the encoded proteins thereof. Specifically, it refers to								
CC	cDNA clones obtained by an oligo-capping method, where none of these								
CC	clones are identical to any known human mRNAs. The present invention								
CC	describes an immunoassay to identify agonists and antagonists, as well as								
CC	antibodies, antisense molecules and siRNAs that can all be used to bind								

to and modulate expression of the cDNA molecules. As such, these molecules are useful for diagnostic markers or therapeutic targets for the various diseases or morbid states. In particular, they are useful in gene therapy for creating osteoporosis, neurological disease, Alzheimer's disease, Parkinson's disease, dementia, short memory and various cancers, as well as for maintaining equilibrium of sense or motor function, and for creating emotional reaction, fear response and panic. Accordingly, they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, cyostatic and tranquilliser activities. This polynucleotide is a full length human cDNA sequence of the invention. NOTE: This sequence is not given in the sequence listing of the specification but can be obtained on CD-ROM from the European Patent Office, Vienna Sub-office.

Sequence 5089 BP; 891 A; 1705 C; 1495 G; 998 T; 0 U; 0 Other;

Query Match 67.5%; Score 316; DB 13; Length 5089;

Best Local Similarity 78.9%; **Pred. No.** 1.3e-80;

Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

5 GAGCTGGCCTTAGAGTCCGGCACTAGTGAATGTGCAGATCCCCCTTGCTCTGGGCCAGCTG 64

Db 610 GTGCTGGCCTTGGGTCCGCACTCGTGATGTACAGATCCCCCTGCTCCTGGCCAGCTG 669

65 GTGAGATTGTCGCCAAGTACACGAGGACCATGGGGAGTTCNTGTGTGANTCCCGN 124

Db 670 GTAGAGTCTGCGCCAGTACACAGGACCACTAGGAGTTTCATGACTGAGTCCAG 729

125 AAGCTCAGCAGCCACTGCTCTACTGACAGGATTGAGGACTGATGACCTTGGATAC 184

Db 730 AATCTCAGCACCCACTGCTTATCTCTATGGTGTCAGGACTGCTGACCTTCGGGTAC 789

185 CTAGTGTCTGTCCACATGNNGANCNCATGGCCATGNACATGGGAAAGCCCTTTC 244

Db 790 CTGCTGCTGCTGCTCCACGTTGGCCGACGATGGCTGTGGACATGCGGAGGCCCTCTTC 849

[illegible][illegible]

D6 850 AGCTCCCGTGTCCGACAGATCACCTCTTTGGGCCCTTATTTCATCCTCAT

305 GAGTCGCTTGACTACTGATGTGCAAGAAATCAAGGCATCCCTTAAAGCTTGCATINCCA 308

Db 909 GAGCCGCTTGACAACTGACGTGACGAGTTTAAGTCATCCTCAAGCTTGTGATCTCCCA 968

365 GGGACTGNGCAGCTGNACCCAGGTGATTGGTAGCCCTGGAGNCCCTGNTATGCTGNCCC 424

Db 969 GGGGCTGCGAAGCTGCACCCAGGTGGCAGGCTGCTGTCCCTGTCCATGCTGTCGAC 102

425 TCGCCTTACCCTGATGCTGGCTGNNGNCAACCCGCCCTCATGG 468

[illegible]

RESULT 7
AAC76613
ID AAC76613 standard; cDNA; 1211 BP.

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AAC76613:

XX 00 FEB 2001 (EST EST ARTTY)

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DE Human ORF1 ORF2188 polynucleotide sequence SEQ ID NO: 1888

KW Human; open reading frame; ORF; detection; cytostatic; hepatotropic; antiviral; antiparkinsonian; nootropic; neuroprotective; vulnervary; antiapoptotic; antiparkinsonian; nootropic; neuroprotective;

KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotonic; antidiabetic;

hypotensive; dermatological; immunosuppressive; antiinflammatory;

KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW antibacterial; antilungal; antineoplastic; antineurotic; antineurotic;
KW antiviral; antibacterial; antilungal; antineoplastic; antineurotic; antineurotic;

KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;

cholesterol ester storage; systemic lupus erythematosus; infection;
kwashiorkor; immunodeficiency; malaria; autoimmune disorder; asthma;
vitamin deficiency

NY 100-104501-104502-104503-104504-104505-104506-104507-104508-104509-104510-104511-104512-104513-104514-104515-104516-104517-104518-104519-104520-104521-104522-104523-104524-104525-104526-104527-104528-104529-104530-104531-104532-104533-104534-104535-104536-104537-104538-104539-104540-104541-104542-104543-104544-104545-104546-104547-104548-104549-104550-104551-104552-104553-104554-104555-104556-104557-104558-104559-104560-104561-104562-104563-104564-104565-104566-104567-104568-104569-104570-104571-104572-104573-104574-104575-104576-104577-104578-104579-104580-104581-104582-104583-104584-104585-104586-104587-104588-104589-104590-104591-104592-104593-104594-104595-104596-104597-104598-104599-104600-104601-104602-104603-104604-104605-104606-104607-104608-104609-104610-104611-104612-104613-104614-104615-104616-104617-104618-104619-104620-104621-104622-104623-104624-104625-104626-104627-104628-104629-104630-104631-104632-104633-104634-104635-104636-104637-104638-104639-104640-104641-104642-104643-104644-104645-104646-104647-104648-104649-104650-104651-104652-104653-104654-104655-104656-104657-104658-104659-104660-104661-104662-104663-104664-104665-104666-104667-104668-104669-104670-104671-104672-104673-104674-104675-104676-104677-104678-104679-104680-104681-104682-104683-104684-104685-104686-104687-104688-104689-104690-104691-104692-104693-104694-104695-104696-104697-104698-104699-104700-104701-104702-104703-104704-104705-104706-104707-104708-104709-104710-104711-104712-104713-104714-104715-104716-104717-104718-104719-104720-104721-104722-104723-104724-104725-104726-104727-104728-104729-104730-104731-104732-104733-104734-104735-104736-104737-104738-104739-104740-104741-104742-104743-104744-104745-104746-104747-104748-104749-104750-104751-104752-104753-104754-104755-104756-104757-104758-104759-104760-104761-104762-104763-104764-104765-104766-104767-104768-104769-104770-104771-104772-104773-104774-104775-104776-104777-104778-104779-104780-104781-104782-104783-104784-104785-104786-104787-104788-104789-104790-104791-104792-104793-104794-104795-104796-104797-104798-104799-104800-104801-104802-104803-104804-104805-104806-104807-104808-104809-104810-104811-104812-104813-104814-104815-104816-104817-104818-104819-104820-104821-104822-104823-104824-104825-104826-104827-104828-104829-104830-104831-104832-104833-104834-104835-104836-104837-104838-104839-104840-104841-104842-104843-104844-104845-104846-104847-104848-104849-104850-104851-104852-104853-104854-104855-104856-104857-104858-104859-104860-104861-104862-104863-104864-104865-104866-104867-104868-104869-104870-104871-104872-104873-104874-104875-104876-104877-104878-104879-104880-104881-104882-104883-104884-104885-104886-104887-104888-104889-104890-104891-104892-104893-104894-104895-104896-104897-104898-104899-104900-104901-104902-104903-104904-104905-104906-104907-104908-104909-104910-104911-104912-104913-104914-104915-104916-104917-104918-104919-104920-104921-104922-104923-104924-104925-104926-104927-104928-104929-104930-104931-104932-104933-104934-104935-104936-104937-104938-104939-104940-104941-104942-104943-104944-104945-104946-104947-104948-104949-104950-104951-104952-104953-104954-104955-104956-104957-104958-104959-104960-104961-104962-104963-104964-104965-104966-104967-104968-104969-104970-104971-104972-104973-104974-104975-104976-104977-104978-104979-104980-104981-104982-104983-104984-104985-104986-104987-104988-104989-104990-104991-104992-104993-104994-104995-104996-104997-104998-104999-105000-105001-105002-105003-105004-105005-105006-105007-105008-105009-105010-105011-105012-105013-105014-105015-105016-105017-105018-105019-105020-105021-105022-105023-105024-105025-105026-105027-105028-105029-105030-105031-105032-105033-105034-105035-105036-105037-105038-105039-105040-105041-105042-105043-105044-105045-105046-105047-105048-105049-105050-105051-105052-105053-105054-105055-105056-105057-105058-105059-105060-105061-105062-105063-105064-105065-105066-105067-105068-105069-105070-105071-105072-105073-105074-105075-105076-105077-105078-105079-105080-105081-105082-105083-105084-

KM allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KM bone damage; cartilage damage; antiinflammatory disease; coagulation;
KM thrombosis; contraceptive; ss.
XX
OS Homo sapiens.
XX
PN WO200058473-A2.
XX
PD 05-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-US008621.
XX
PR 31-MAR-1999; 99US-0127607P.
PR 02-APR-1999; 99US-0127636P.
PR 05-APR-1999; 99US-0127728P.
PR 30-MAR-2000; 2000US-00540763.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI, 2000-602362/57.
DR P-PSDB; AAB42404.
XX
XX Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease.
XX
PS Claim 5; Page 3530-3531; 5507pp; English.
XX
XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
CC antipariatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
CC cardiatic; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
CC dermatological; immunosuppressive; antiinflammatory; antibacterial;
CC antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
CC sequences can be used for determining the presence of or predisposition
CC to, or preventing or treating pathological conditions associated with an
CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
CC proteins in gene therapy vectors. The proteins and nucleic acids may be
CC used to treat cancers, proliferative disorders, neurodegenerative
CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
CC storage, systemic lupus erythematosus, severe combined immunodeficiency
CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
CC enhance coagulation; to inhibit thrombosis; and as a contraceptive
XX
SQ Sequence 1211 BP; 228 A; 372 C; 358 G; 253 T; 0 U; 0 Other;
Query Match 67.3%; Score 315; DB 3; Length 1211;
Best Local Similarity 78.8%; Pred. No. 1.5e-80;
Matches 365; Conservative 0; Mismatches 97; Indels 1; Gaps 1;
QY 6 AGCTGGCCTTAGTGCGGCACTAGTGAATGTCAGATCCCTTGCTCTGGCCAGCTGG 65
DB 119 AGCTGGCCTTAGTGCGGCACTGTAATGTACAGATCCCCCTGCTCTGGCCAGCTGG 178
QY 66 TGGAGATTGTGCGCAAGTACACGAGGACCATGGGAGTNTGNTGANTCCCGNA 125
DB 179 TAGAGGTGCTGGCCAAGTACACAAGGACCAAGTAGGAGTTTCACTAGTCTCAGA 238
QY 126 AGCTCAGCNCANCTGCTCTACTGNACNGAGTTACAGNACTGNTGACCTTNGATACC 185
DB 239 ATCTCAGACACCACTGCTTATCTCTATGTGTCCAGGACTGTGACCTTGGGTACC 298
QY 186 TAGTGTGCTGTCCCAATGNNGANCNCATGGCCATGNACATGGGAAAGCCCTTTTCA 245
DB 299 TGGTGTGCTGTCTCCACGTGGCGGAGCGCATGCTGTGACATGCGGAGGCCCTTTCA 358

QY 246 GCTCCCTGCTCCGCAAGACATGCTTTNTTGATGCCAAAAGACAGGCGTAGTG 305
DB 359 GCTCCCTGCTCCGCAAGACATCACCCTTTTGACGCCAATGAAGACAGGCGAGC-7G6TG 417
QY 306 AGTGCCTGACTAGTATGTGCAAGAATTCAAGGCATCCTTNAAGCTTGTCATNTCCAG 365
DB 418 AGCCGCTTGACAAGTACAGTGCAGAGGTTAAGTCATCCTTCAAGCTTGTCATCCAG 477
QY 366 GACTGNGCAGCTGNACCCAGGTGATTGCTAGCCTGAGNCCCTGNTATGCTGNCCTT 425
DB 478 GGGCTGCGAAGCTGCACCCAGGTGGAGGCTGCTGTGTCTTCATGTCTGCACA 537
QY 426 CGCCTTACCCTGATGTGCTGCTGNNNGACACCCGCCCTCATGG 468
DB 538 CGCCTCAGCTGTGCTGTGATGTGTGCCACACAGCCCTGATGG 580
RESULT 8
AAH18672
ID AAH18672 standard; cDNA; 2383 BP.
XX
AC AAH18672;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:18919.
XX
KM Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI, 2001-318749/34.
XX
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
XX cDNAs.
PS Claim 8; SEQ ID NO 18919; 2537pp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by

CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention

XX Sequence 2383 BP; 405 A; 767 C; 745 G; 466 T; 0 U; 0 Other;

Query Match 64.6%; Score 302.4; DB 4; Length 2383;
Best Local Similarity 78.4%; Pred. No. 8.4e-77;
Matches 364; Conservative 0; Mismatches 98; Indels 2; Gaps 2;

OY 5 GAGCTGGCCTTAGTGGCGCACTGATGTGACAGATCCCTTGTCTCTGGGCCAGCTG 64
DB 420 GTGCTGGCCTTGGGTGGCGCACTGTGAATGTACAGATCCCCCTGTCTCTGGGCCAGCT- 478
OY 65 GTGAGATTGTCCGCAAGTACACGAGGAGCCACATGGGGAGNTGNTGANTCCCGN 124
DB 479 GTAGAGGTGTGGCCCAAGTACACAGAGGAGCCAGTAGGAGTTTCATGACTGATGCCAG 538
OY 125 AAGCTCANGNCCANCTGCTCTCTACTGACNAGAGTTCAAGNACTGNTGACCTTNGATAC 184
DB 539 AATCTCAGCACTCACTGCTTATCTCTATGTGTCCAGGAGCTGTGACCTTCCGGGTAC 598
OY 185 CTAGTGTGCTGTCCACATTGNNGANCATGGCCATGNAATGCGGAAAGCCCTTTTC 244
DB 599 CTGCTGTGCTGTCCACATTGNNGANCATGGCCATGNAATGCGGAAAGCCCTTTTC 658
OY 245 AGCTCCCTGTCTCCGCAAGACATGCTTNTTGTATGCAAAAGACAGGCGAGCTAGT 304
DB 659 AGCTCCCTGTCTCCGCAAGACATGCTTNTTGTATGCAAAAGACAGGCGAGCTAGT 717
OY 305 GAGTGGCTGACTACTGATGTGCAAGAATTCAAGGATCCTTNAAGCTTGTCAATTNCCA 364
DB 718 GAGCCGCTTGACAACTGACGTGCAAGAGTTTAAGTCATCTTCAAGCTTGTCAATCCCA 777
OY 365 GGGACTGNGCAGCTGNACCCAGGTGATGTTGCTGAGNCCCTGNTATGCTGNCCC 424
DB 778 GGGGCTGCGAAGCTGCACCCAGGTGAGGCTGCTGTGTCTCTGTCATGCTGTGCAC 837
OY 425 TCGCCTTACCTGATGCTGCTGNNNGNACACCCGCCCTCATGG 468
DB 838 ACGCCTCAGCTGCTGCTGATGTGTGCCACACAGCCCTGATGG 881

RESULT 9
AAA62022 standard; DNA; 1251 BP.

XX AAA62022;
DT 02-FEB-2001 (first entry)

XX Hydrophobic domain protein cDNA HP10628 isolated from HT-1080 cells.

XX Human; secreted protein; membrane protein; hydrophobic domain;
XX proliferation control; differentiation induction; material transport;
XX biophylaxis; signal receptor; ion channel; transporter; immunostimulant;
XX immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic;
XX haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
XX autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer;
XX gene therapy; 88.

OS Homo sapiens.

PN WO200029448-A2.

PD 25-MAY-2000.

PF 17-NOV-1999; 99WO-JP006412.

XX 17-NOV-1998; 98JP-00326255.

PR 22-DEC-1998; 98JP-00364315.
PR 16-MAR-1999; 99JP-00069811.
PR 27-APR-1999; 99JP-00119299.
PR 19-MAY-1999; 99JP-00138169.
XX (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
XX Kato S, Kilmura T;
PI
XX WPI; 2000-387753/33.
DR P-PSDB; AAB12139.
DR

PT Proteins comprising hydrophobic regions, such as secretory and membrane
PT proteins, useful in research and diagnostics and having various
PT activities e.g. immunomodulatory, antiinflammatory, chemokinetic,
PT hemostatic, thrombolytic.

PS Claim 3; Page 301; 410pp; English.

CC Secretory proteins play important roles in the proliferation control, the
CC differentiation induction, the material transport and the biophylaxis of
CC cells. Membrane proteins have important roles as signal receptors, ion
CC channels and transporters. The present sequence is the coding sequence
CC for a human protein which has at least one hydrophobic domain. The
CC protein encoded by the present sequence may be a secretory or a membrane
CC protein. The encoded protein may have cytokine and cell
CC proliferation/differentiation activity, immune stimulating or suppressing
CC activity, haematopoiesis activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, anti-inflammatory activity and tumour
CC inhibition activity. The present sequence could therefore be used for
CC treatment of autoimmune disease, Alzheimer's disease, Parkinson's
CC disease, and cancer via gene therapy

XX Sequence 1251 BP; 204 A; 394 C; 385 G; 268 T; 0 U; 0 Other;

Query Match 59.3%; Score 277.6; DB 3; Length 1251;
Best Local Similarity 74.3%; Pred. No. 9.7e-70;
Matches 367; Conservative 0; Mismatches 96; Indels 31; Gaps 2;

OY 5 GAGCTGGCCTTAGTGGCGCACTAGTGAATGTGACAGATCCCTTGTCTCTGGGCCAGCTG 64
DB 406 GTGCTGGCCTTGGGTGGCGCACTGTGAATGTACAGATCCCCCTGTCTCTGGGCCAGCTG 465
OY 65 GTGAGATTGTCCGCAAGTACACGAGGAGCCACATGGGGAGNTGNTGANTCCCGN 124
DB 466 GTAGAGGTGTGGCCCAAGTACACAGAGGAGCCAGTAGGAGTTTCATGACTGATGCCAG 525
OY 125 AAGCTCANGNCCANCTGCTCTCTACTGACNAGAGTTCAAGNACTGNTGACCTTNGATAC 184
DB 526 AATCTCAGCACTCACTGCTTATCTCTATGTGTGTCCAGGAGCTGTGACCTTCCGGGTAC 585
OY 185 CTAGTGTGCTGTCCACATTGNNGANCATGGGCCATGNAATGCGGAAAGCCCTTTTC 244
DB 586 CTGCTGTGCTGTCCACATTGNNGANCATGGGCCATGNAATGCGGAAAGCCCTTTTC 645
OY 245 AGCTCCCTGTCTCCG-----CAGACATTGCTTN 274
DB 646 AGCTCCCTGTCTCCGCTACTGCGACGCCGAGGTGACAGATTGGGACAAAGACATCACTTC 705
OY 275 TTTGATGCCAAAAGACAGGCGAGGTAGTAGTGGTTGACTGATGTGCAAGAAAT 334
DB 706 TTTGACGCCAAATAAGACAGGCGAGC-TGGTAGCCGCTTGACAACTGACGTGCAAGAGTT 764
OY 335 CAAGGCATCTTNAAGCTTGTCAATTNCCAGGAGCTGNGCAGCTGNACCCAGGTGATTGG 394
DB 765 TAAGTCACTCTTCAAGCTTGTCACTTCCAGGGGCTGCAAGCTGCAACCAAGTGGCAGG 824
OY 395 TAGCCTGAGNCCCTGNTATGCTGNCCCTGCTTACCTGATGCTGCTGCTGNNNGAC 454
DB 825 CTGCTGTGTCTCTGTCCATGCTGTGACACGCTTACGCTGCTGCTGATGTGTGCCAC 884

QY 455 ACCCGCCCTCATGG 468
Db 885 ACCAGCCCTGATGG 898

RESULT 10
AAA62032
ID AAA62032 standard; DNA; 1617 BP.

XX AAA62032;

DT 02-FEB-2001 (first entry)

XX Hydrophobic domain protein cDNA HP10628 isolated from HT-1080 cells.

KM Human; secreted protein; membrane protein; hydrophobic domain;
KM proliferation control; differentiation induction; material transport;
KM biophylaxis; signal receptor; ion channel; transporter; immunostimulant;
KM immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic;
KM haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
KM autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer;
KM gene therapy; ss.

OS Homo sapiens.

PN WO200029448-A2.

PD 25-MAY-2000.

XX 17-NOV-1999; 99WO-JP006412.

PR 17-NOV-1998; 98JP-00326255.

PR 22-DEC-1998; 98JP-00364315.

PR 16-MAR-1999; 99JP-00069811.

PR 27-APR-1999; 99JP-00119299.

PR 19-MAY-1999; 99JP-00138169.

XX (SAGA) SAGAMI CHEM RES CENT.

PA (PROT-) PROTEGENE INC.

PI Kato S, Kimura T;

XX WPI; 2000-387753/33.

DR P-PSDB; AAB12139.

PT Proteins comprising hydrophobic regions, such as secretory and membrane
PT proteins, useful in research and diagnostics and having various
PT activities e.g. immunomodulatory, antiinflammatory, chemokinetic,
hemostatic, thrombolytic.

PS Claim 4; Page 313-316; 410pp; English.

CC Secretory proteins play important roles in the proliferation control, the
CC differentiation induction, the material transport and the biophylaxis of
CC cells. Membrane proteins have important roles as signal receptors, ion
CC channels and transporters. The present sequence is the coding sequence
CC for a human protein which has at least one hydrophobic domain. The
CC protein encoded by the present sequence may be a secretory or a membrane
CC protein. The encoded protein may have cytokine and cell
CC proliferation/differentiation activity, immune stimulating or suppressing
CC activity, haematopoiesis activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, anti-inflammatory activity and tumour
CC inhibition activity. The present sequence could therefore be used for
CC treatment of autoimmune disease, Alzheimer's disease, Parkinson's
CC disease, and cancer via gene therapy

XX Sequence 1617 BP; 293 A; 504 C; 465 G; 355 T; 0 U; 0 Other;

Query Match 59.3%; Score 277.6; DB 3; Length 1617;
Best Local Similarity 74.3%; Pred. NO. 1.1e-69;
Matches 367; Conservative 0; Mismatches 96; Indels 31; Gaps 2;

QY 5 GAGTGGCCTTAGTGGCGCACTAGTGAATGTGAGATCCCTTGTCTCTGGGCCAGCTG 64
Db 472 GTGCTGGCCTTGGGTGGCGCACTGTGAATGTACAGATCCCTGTCTCTGGGCCAGCTG 531

QY 65 GTGAGATTGTGCGCAAGTACAGAGGACCACTGGGAGTNCNTGTNTGANTCCCGN 124

Db 532 GTAGAGGTGTGGCCAAGTACAGAGGACCACTGGGAGTTCATGACTGATGCCAG 591

QY 125 AAGTCAGNCCNCTGCTCTACTGNACNAGTTCAGNACTGNTGACCTTNGATAC 184

Db 592 AATCTGAGACCCACTGTATCTCTATGTGTCCAGGAGTGTGACCTTCCGGTAC 651

QY 185 CTAGTGTCTGTCTCCACATTTGNNGANCATGGCCATGNACATGCGGAAGCCTTTTC 244

Db 652 CTGCTGTCTGTCTCCACGTTGGCGGACATGGCTGTGACATGCGGAGGCTCTTC 711

QY 245 AGCTCCCTGCTCCG-----CAAGACATTGCTTTN 274

Db 712 AGCTCCCTGCTCCGTTACTGCCAGCCGAGGTGCAGAGTTGGACAAAGACATCACTTC 771

QY 275 TTTGATGCCAAAAGACAGGCGAGCTAGTGTGCTGACTGATGTGCAAGAATT 334

Db 772 TTTGACGCCAATAAGACAGGCGAGC-TGGTAGCCGCTTGACAACGTGACGAGATT 830

QY 335 CAAGGACCTTNAAGCTTGTCATNTNCCAGGAGCTGNCAGCTGNACCCAGGTATTG 394

Db 831 TAAGTCATCTTCAAGCTTGTGATCTCCAGGGCTGCGAAGCTGACCCAGGTGGCAGG 890

QY 395 TAGCCTGAGNCCCTGNTATGTGNCCTGCTGCTTACCTGATGCTGGCTGNNNCAC 454

Db 891 CTGCTGTGTCTCCTGTCCATGTCTGTGACACGCTTCACGCTGTCTGATGTGTGCCAC 950

QY 455 ACCCGCCCTCATGG 468

Db 951 ACCAGCCCTGATGG 964

RESULT 11

ACN41861

ID ACN41861 standard; cDNA; 2317 BP.

XX ACN41861;

DT 18-NOV-2004 (first entry)

XX Human diagnostic and therapeutic polynucleotide SEQ ID NO:736.

XX ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;
KM dithp.

OS Homo sapiens.

XX WO2004023973-A2.

PD 25-MAR-2004.

XX 12-SEP-2003; 2003WO-US028227.

PR 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,

PI Harthorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV;

PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;

PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LJ;

PI Lagace RE, Spiro PA, Stewart RA, Wingrove J, Vilt UA, Kirton ES;

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

PI Patuay S, Shi X, Suarez CJ;

DR WPI; 2004-329368/30.

DR P-PSDB; ABM83209.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 1, Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp polynucleotide of
CC the invention. Note: The sequence data for this patent is not represented
CC in the printed specification, but was obtained in electronic format
CC directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 2317 BP; 400 A; 729 C; 737 G; 451 T; 0 U; 0 Other;
Query Match 49.1%; Score 230; DB 13; Length 2317;
Best Local Similarity 67.8%; Pred. No. 7.2e-56;
Matches 366; Conservative 0; Mismatches 97; Indels 77; Gaps 2;
QY 5 GAGCTGGCCTTAGGTGGTGGCACTAGTGAATGTGCAGATCCCTTGTCTCTGGGCCAGCTG 64
DB GTGCTGGCCTTGGGTGGTGGCACTAGTGAATGTGCAGATCCCTTGTCTCTGGGCCAGCTG 546
QY 65 GTGAGATTGTGCGCAAGTACACGAGGACCAATGGGAGTNTGTTGANTCCCN 124
DB GTAGAGTGTGGCGCAAGTACACAGGAGCACGTAAGGAGTTTCATGACTGAGTCCAG 606
QY 125 AAGCTCANGNCANCTGCTCTACTGNA CNGAGTT----- 160
DB AATCTCAGCACCACTGCTTATCTCTATGTGTCTCAGGTACAGCCGGAGTGGGCTG 666
QY 161 -----CAGNACT 168
DB GGGACCGCCGAGGAGCCACCCGAGGCATCCCTGAGTGCATGGGCTCTTCCGACGGACT 726
QY 169 GNTGACCTTNGATACCTAGTGTCTGTGCCACATTGNNGANGNCATGGCCATGNACAT 228
DB GCTGACCTTGGGTACCTGTGTCTGTCTGCCACGTTGGCGAGCGCATGGCTGTGACAT 786
QY 229 GCGAAGGCCCTTTTCAGCTCCCTGTCCGCGCAAGACATTGCTTNTTGTATGCCAAAA 288
DB GCGGAGGGCCCTCTTCACTCCCTGTCCGACAAGACATCACTTCTTGACGCCAATTA 846
QY 289 GACAGGGCAGCGTAGTGTGCTTGAATACTGATGTGCAAGAAATCAAGGCATCCTTNA 348
DB GACAGGGCAGC-TGGTAGCCGCTTGACAATGACGTGACAGAGTTTAAATCATCTTCA 905
QY 349 AGCTTGTCAATNCCAGGAGCTGNGACGTGNACCCAGGTGATGGTAAAGCTGAGNCCC 408
DB AGCTTGTCAATCTCCAGGGGCTGCGAAGCTGCACCCAGGTGCGAGGCTGCTGTGCC 965
QY 409 TGNNTATGCTGNCCCTCGCCTTACCCCTGATGCTGGCTGNNNGNCAACCCGCCCTCATGG 468
DB TGTCCATGCTGTGACACGCCCTCAGCTGTCTGTGATGTGGCCACACCAAGCCCTGATGG 1025

RESULT 12
ABL89954
ID ABL89954 standard; cDNA; 1805 BP.
XX

AC ABL89954;
XX
DT 24-MAY-2002 (first entry)
XX
DE Human polynucleotide SEQ ID NO 516.
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200190304-A2.
XX
PD 29-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-US016450.
XX
PR 19-MAY-2000; 2000US-0205515P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-122018/16.
DR P-PSDB; ABB89545.
XX
PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive,
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders.
XX
PS Claim 4; SEQ ID NO 516; 2081pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABL89449-ABL90853) and proteins
CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1805 BP; 330 A; 558 C; 568 G; 338 T; 0 U; 11 Other;
Query Match 46.9%; Score 219.6; DB 6; Length 1805;
Best Local Similarity 75.8%; Pred. No. 6.6e-53;
Matches 263; Conservative 0; Mismatches 83; Indels 1; Gaps 1;
QY 122 CGAAGCTCANGNCANCTGCTCTACTGNACNGAGTTCAAGNACTGNTGACCTTNGA 181
DB CAGAAATCTCAGACACCCACCTGCTTATCTCTATGTGTGTCAGGAGACTGCTGACCTTGGG 60
QY 182 TACCTAGTGTCTGTGCCACATGNNGANGNCATGGCCATGNACATGCGGAAGCCCTT 241
DB TACCTGTGTGTCTGTGCCACGTTGGCGAGCGCATGGCTGTGACATGCGAGGCTTC 120
QY 242 TTCAGCTCCCTGCTCCGCAAGACATTGCTTNTTGTATGCCAAAAAGACAGGCGCT 301
DB TTCAGCTCCCTGCTCCGCAAGACATCACTTCTTGTAGCGCAATAAGACAGGCGAGC-T 179
QY 302 AGTAGTCGCTTGACTACTGATGTGCAAGAAATCAAGGCACTCTTNAAGCTTGTCAATTN 361

Db 180 GGTAGCGCGCTTGACACTGACGTGACAGAGTTAAGTCATCCTTCAAGCTGTGATCTC 239
QY 362 CCAGGAGTNGCAGCTGNACCCAGGTGATGTGCTGAGNCCCTGNNATATGCTGNC 421
Db 240 CCAGGGGCTGCGAANTGACACCCAGGTGGCAGGCTGCTGTGTCTCTGTCATGCTGTC 299
QY 422 CCCTGCGCTTACCCCTGATGCTGGCTGNNNGACACCCCGCCCTCATGG 468
Db 300 GACACGCGCTCACGNTCTGCTGATGTGTGGCCACACCGCCCTGATGG 346

RESULT 13
ACH43729
ID ACH43729 standard; cDNA, 494 BP.

AC ACH43729;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human foetal brain cDNA #4454.
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KM genome mapping; biodiversity; genetic disorder.
XX Homo sapiens.
OS
XX US2003073623-A1.
PN
XX 17-APR-2003.
PD
XX 30-JUL-2001; 2001US-00918995.
PF
XX 30-JUL-2001; 2001US-00918995.
PR
XX 30-JUL-2001; 2001US-00918995.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
XX WPI; 2003-615964/58.

PT New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.

PS Claim 1; SEQ ID NO 30941; 44pp; English.

XX
CC The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=2003073623

XX Sequence 494 BP; 84 A; 158 C; 135 G; 108 T; 0 U; 9 Other;

Query Match 44.2%; Score 206.8; DB 9; Length 494;

Best Local Similarity 80.1%; Pred. No. 2e-49;
Matches 229; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 5 GAGTGGCCTTAGGTGGCGCACTAGTGAATGTGAGATCCCTTGCTCTGGCCAGCTG 64
Db 208 GTGCTGGCCTTGAGGTGCGGCACTCGTAATGTACAGATCCCTGCTCTGGCCAGCTG 267
QY 65 GTGAGATTGTGCCCAAGTACACGAGGACCATATGGGGAGTNCNTGTNTGANTCCCGN 124
Db 268 GTAGAGGTGTTGGCCAAAGTACACAAAGGACCAAGTAGGAGTTTCATGACTGAGTCCAG 327
QY 125 AAGCTCAGCAGCCAGCTGCTCTACTGNAAGAGTTGAGNACTGNTGACCTTNGATAC 184
Db 328 AATCTCAGCACCACTGCTTATCTTATGTGTGTCAGGAGCTGCTGACCTTCGGGTAC 387
QY 185 CTAGTCTGCTGTCCCAACATTGNNAGNCATGGCCATGACATGCGAAAGCCCTTTC 244
Db 388 CTGCTGCTGTGTCCACGTTGGCGAGCGCATGGCTGTGACATGCGAGGAGCCCTCTTC 447
QY 245 AGCTCCCTGCTCCGCAAGACATGCTTNTTTGATGCCAAAGA 290
Db 448 AGCTCCCTGCTCCGCAAGACATGCTTNTTTGATGCCAAAGA 493

RESULT 14
AAF22411
ID AAF22411 standard; cDNA, 1023 BP.

AC AAF22411;
XX
DT 26-MAR-2001 (first entry)
XX
DE Human secreted protein gene 39 SEQ ID NO:49.

XX
KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm;
KW rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;
KW cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia;
KW angiogenesis; nervous system disorder; Alzheimer's disease; infection;
KW ocular disorder; corneal infection; wound healing; skin aging;
KW food additive; preservative; ss.

OS Homo sapiens.
XX
XX WO200061629-A1.

PN 19-OCT-2000.

PD 06-APR-2000; 2000WO-US009071.

PF 09-APR-1999; 99US-0128694P.
XX
PR 20-JAN-2000; 2000US-0176931P.

PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.

XX
PI Ruben SM, Komatsoulis G;
XX
XX WPI; 2000-647420/62.
DR P-PSDB; AAB63172.

DR
XX Isolated nucleic acid molecule encoding a human secreted protein is used
PT in preventing, treating or ameliorating a medical condition.

PT
XX Claim 1; Page 450-451; 533pp; English.

XX
CC AAF22373 to AAF22421 encode the human secreted proteins given in AAB63134
CC to AAB63182. AAB63183 to AAB63231 represent more human secreted proteins
CC and polypeptides homologous to them. Human secreted proteins have
CC activities based on the tissues and cells the genes are expressed in.
CC Examples of activities include: immunosuppressive; antiarthritic;

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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 19:56:09 ; Search time 3081 Seconds
(without alignments)
7106.899 Million cell updates/sec

Title: US-10-327-713-267
Perfect score: 468
Sequence: 1 gactgagctggccttagtg.....ngncacacccgccctcatgg 468

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gsa1:*
10: gb_gsa2:*
11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	436	93.2	468	10	CG663507	CG663507 OST448795
2	415	88.7	751	6	CB249142	CB249142 UI-M-FC0-
3	415	88.7	1659	4	AK014688	AK014688 Mus muscu
4	415	88.7	2154	10	AY407420	AY407420 Mus muscu
5	415	88.7	2647	4	AK049152	AK049152 Mus muscu
6	415	88.7	2669	4	AK038760	AK038760 Mus muscu
7	415	88.7	2676	4	AK014319	AK014319 Mus muscu
8	415	88.7	2779	4	AK030624	AK030624 Mus muscu
9	414	88.5	780	6	CA945430	CA945430 UI-M-FD0-
10	411.8	88.0	2699	4	AK076315	AK076315 Mus muscu
11	400.2	85.5	553	8	CX211935	CX211935 MNS16502
12	392.8	83.9	771	2	BI147958	BI147958 602912678
13	329.2	70.3	750	6	CF726195	CF726195 UI-M-GZ0-
14	321.2	68.6	628	3	BI738314	BI738314 603361553
15	317.6	67.9	4340	3	CR857093	CR857093 Pongo pyg
16	316	67.5	572	4	BQ189757	BQ189757 UI-E-EJ1-
17	316	67.5	625	3	BM783111	BM783111 K-EST0060
18	316	67.5	674	3	BM930206	BM930206 UI-E-EJ1-
19	316	67.5	1484	4	CR599833	CR599833 full-leng
20	316	67.5	1553	4	CR610778	CR610778 full-leng
21	316	67.5	1553	4	CR616094	CR616094 full-leng
22	316	67.5	1594	4	CR592221	CR592221 full-leng

23	316	67.5	1625	4	CR595185	CR595185 full-leng
24	316	67.5	2157	10	AY407418	AY407418 Homo sapi
25	311.8	66.6	2143	10	AY407419	AY407419 Pan trogl
26	310	66.2	1067	3	BQ226274	BQ226274 AGENCOURT
27	306.4	65.5	954	5	BX386624	BX386624 AGENCOURT
28	305.6	65.3	861	6	CA751818	CA751818 UI-M-FD0-
29	304	65.0	822	6	CF731448	CF731448 UI-M-GZ0-
30	293.8	62.8	580	3	BP269263	BP269263 BP269263
31	293.6	62.7	932	1	AL583448	AL583448 AL583448
32	289.8	61.9	962	1	AL561411	AL561411 AL561411
33	289	61.8	961	1	AL556542	AL556542 AL556542
34	284.6	60.8	574	3	BP203165	BP203165 BP203165
35	284.2	60.7	1042	5	BX375231	BX375231 BX375231
36	282.6	60.4	762	3	BM943684	BM943684 UI-M-EH0P
37	282.2	60.3	778	3	BI650183	BI650183 603296274
38	281	60.0	886	5	BU501235	BU501235 AGENCOURT
39	279.6	59.7	1043	3	BI650435	BI650435 603296174
40	273.4	58.4	886	1	AL555395	AL555395 AL555395
41	269.8	57.6	599	2	BE284252	BE284252 601087307
42	267.2	57.1	769	1	AU079920	AU079920 AU079920
43	266.8	57.0	1134	1	AL571863	AL571863 AL571863
44	264.4	56.5	621	3	BI549942	BI549942 603194789
45	262.6	56.1	958	1	AL546553	AL546553 AL546553

ALIGNMENTS

RESULT 1	CG663507	468 bp	mRNA	linear	GSS 02-OCT-2003							
LOCUS	OST448795	Mus musculus	129Sv/Ev	Mus musculus	CDNA clone OST448795,							
DEFINITION	mRNA sequence.											
ACCESSION	CG663507											
VERSION	CG663507.1	GI:37487356										
KEYWORDS	GSS.											
SOURCE	Mus musculus	(house mouse)										
ORGANISM	Mus musculus											
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.											
AUTHORS	1 (bases 1 to 468) Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J., Piggott,J., BeltrandelRio,H., Buxton,B.C., Edwards,J., Finch,R.A., Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.											
TITLE	wnt1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention											
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	100 (24)	14109-14114	(2003)								
PUBMED	14610273											
COMMENT	Contact: Zambrowicz BP Omnibank Lexicon Genetics Incorporated 4000 Research Forest Drive, The Woodlands, TX 77381, USA Email: materials@lexgen.com Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11) Class: Gene Trap.											
FEATURES	Location/Qualifiers											
source	1..468 /organism="Mus musculus" /mol_type="mRNA" /strain="129Sv/Ev" /db_xref="taxon:10090" /clone="OST448795" /cell_type="embryonic stem cell" /clone_lib="Mus musculus 129Sv/Ev"											
ORIGIN												
Query Match	93.2%	Score 436;	DB 10;	Length 468;								

TITLE	JOURNAL	PUBMED	REFERENCE	AUTHORS
High-efficiency full-length cDNA cloning	Meth. Enzymol. 303, 19-44 (1999)	10349636		Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Genome Res. 10 (10), 1617-1630 (2000)	11042159		3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer	Genome Res. 10 (11), 1757-1771 (2000)	11076861		4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	Functional annotation of a full-length mouse cDNA collection	Nature 409, 685-690 (2001)		5
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	Nature 420, 563-573 (2002)		6 (bases 1 to 1659)
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.				
Direct Submission	Submitted (10-JUL-2000)			
Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)				
Please visit our web site (http://genome.gsc.riken.jp/) for further details.				
cdna library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTAATTAATATCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised longer than 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.				
Location/Qualifiers				

```

source
    1. .1659
        /organism="Mus musculus"
        /mol_type="mRNA"
        /strain="C57BL/6J"
        /db_xref="PANTOM_DB:4833412N02"
        /db_xref="taxon:10090"
        /clone="4833412N02"
        /tissue_type="head"
        /clone_1ib="RIKEN full-length enriched mouse cDNA library"
        /dev_age="0 day neonate"
        1. .1659
            /note="ATP-binding cassette, sub-family B (MDR/TAP)",
            member 8 (MGD|GDI:1351667, GB|AF213391, evidence: BLASTN,
            99%, match=370)"

misc_feature

ORIGIN

Query Match      88.7%; Score 415; DB 4; Length 1659;
Best Local Similarity 91.9%; Pred.No. 2.8e-107;
Matches 429; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

QY      2   ACTGAGCTGGCCCTTAGGTGGCGCACTAGTGAATGTGCAGATCCCCTTGCTCTGGCCAG 61
         |||||||||
Db       493 ATTGTGCTGGCCCTTAGGTGGCGCACTAGTGAATGTGCAGATCCCCTTGCTCTGGCCAG 552

QY      62   CTGTGTGAGATTGTTCGCCAAGTAACAGAGGGACCACATGGGGAGNTNCNTGTNTGANTCC 121
         |||||||||
Db       553 CTGTGTGAGATTGTTCGCCAAGTAACAGAGGGACCACATGGGGAGTTTCGTGTCTGAGTCC 612

QY      122  CGNAAGCTCANCGNCCANCTGCTCTACTGNACNGAGTTCAAGNACTGNTGACCTTTGGA 181
         |||||||||
Db       613 CGTAAGCTCACGCTCCAGCTGCTCTACTGTACGCTGTTCAAGGACTGTGACCTTTGGA 672

QY      182  TACCTAGTGTGCTGTGCCCATTTGNNGANCNATGGCCATGNACATGCGAAAGCCCTT 241
         |||||||||
Db       673 TACCTAGTGTGCTGTGCCCATTTGNTGTGAGCGCATGGCCATGGAATGCGAAAGCCCTT 732

QY      242  TTCAAGCTCCCTGCTCCGGCAAGACATTGCTTTNTTTGATGCCAAAGAAGACAGGGCAGCGT 301
         |||||||||
Db       733 TTCAGCTCCCTGCTCCGGCAAGACATTGCTTTCTTTGATGCCAAAGAAGACAGGGCAGC-T 791

QY      302  AGTGAAGTGGCTTGAATACTGATGTGCAAGAATTCAAGGCATCTTTNAAAGCTTGATNTN 361
         |||||||||
Db       792 AGTGAAGTGGCTTGAATACTGATGTGCAAGAATTCAAGTCATCTTTCAAGCTTGATNTN 851

QY      362  CCAAGGACTGNGCAGCTGNAAGCCAGGTGATTGTGAGCTGAGNCCCTGMNTATGCTGNC 421
         |||||||||
Db       852 CCAAGGACTGCGCAGCTGCACCCAGGTGATTGTGAGCTGAGTCCCTGTCTATGCTGTC 911

QY      422  CCCTGCGCCTTACCCCTGATGCTGGCTGANNNGACACACCCGCCCTCATGG 468
         |||||||||
Db       912 CCCTGCGCCTTACCCCTGATGCTGGCTGCTGTCACACCCGCCCTCATGG 958

RESULT 4
AY407420          2154 bp      DNA           linear      GSS 15-Dec-200
LOCUS             Mus musculus ABCB8 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION        genomic survey sequence.
ACCESSION         AY407420
VERSION           AY407420.1 GI:39763391
KEYWORDS
SOURCE
ORGANISM          Mus musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS           Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
                  Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
                  Ferrieres,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
                  Adams,M.D. and Cargill,M.
TITLE             Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
```

JOURNAL	Science 302 (5652), 1960-1963 (2003)
PUBMED	14671302
REFERENCE	2 (bases 1 to 2154)
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Clevello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J., Adams, M.D. and Cargill, M.
TITLE	Direct Submission
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES	<p>location/Qualifiers</p> <p>1..2154</p> <p>/organism="Mus musculus"</p> <p>/mol_type="genomic DNA"</p> <p>/db_xref="taxon:10090"</p> <p><1..>2154</p> <p>/gene="ABCB8"</p> <p>/locus_tag="HGM2884"</p>
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Best Local Similarity	91.9%; Pred. No. 3e-107;
Matches	429; Conservative 0; Mismatches 37; Indels 1; Gaps 1;
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ACCESSION	AK049152
VERSION	AK049152.1 GI:26339815
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
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REFERENCE
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE
AUTHORS 2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE
AUTHORS 3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
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Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system-384-Format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE
AUTHORS 4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
PUBMED 11076861
REFERENCE
AUTHORS 5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12002000
REFERENCE
AUTHORS 6 (bases 1 to 2647)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
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Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
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ORIGIN

Query Match	88.7%;	Score 415;	DB 4;	Length 2647;
Best Local Similarity	91.9%;	Pred. No. 3.1e-107;		
Matches 429;	Conservative	0;	Mismatches 37;	Indels 1;
				Gaps 1;

Oy	2	ACTGAGCTGGCCCTTAGGTAGGTGCGGCACTAGTGAATGTGCAGATCCCTTGCTCCTGGGCGAG	61
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Oy	62	CTGTGTGAGATTGTGCGGCAAGTACACGAGGGACCCACATGGGGAGTNTCNTGTNTGANTCC	121
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Oy	122	CGNAAGCTCANCNCNCNCTGCTCCTACTGNACNAGTTCAGGNACTGNTGACCTTNGGA	181
Db	604	CGTAAGCTCAGCGTCCAGCTGCTCCTACTGTACGGTGTTCAGGGACTGTGACCTTTGGA	663
Oy	182	TACCTAGTGTGCTGTGCCACATTGNNGANCNATGGCCATGNACATGCGGAAAGCCCTT	241
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Oy	242	TTGAGCTCCCTGCTCCGGCAAGACATTGCTTTNTTTGATGCCAAAAAGACAGGGCAGCGT	301
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Oy	422	CCCTGCGCTTACCCTGATGCTGGCTGNNNGNACACACCCGCGCTCATGG	468
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LOCUS	
DEFINITION	AK038760 Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230060K10 product:ATP-binding cassette, sub-family B (MDR/TAP), member 8, full insert sequence.
ACCESSION	AK038760
VERSION	AK038760.1 GI:26086722
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1
AUTHORS Carminci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)

REFERENCE
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

TITLE

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the

TITLE	JOURNAL	REFERENCES
Functional annotation of a full-length mouse cDNA collection	Nature 409, 685-690 (2001)	5

JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 2669)
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., ...

TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of

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Best Local Similarity	91.9%	Pred. No. 3.1e-107;		
Matches 429; Conservative	0;	Mismatches 37;	Indels 1;	Gaps 1;

QY	2	ACTGAGCTGGCCCTTAGGTGCGGCACTAGTGAATGTGCAGATCCCTTGCTCCTGGGCCAG	61
Db	467	ATTGTGCTGGCCCTTAGGTGCGGCACTAGTGAATGTGCAGATCCCTTGCTCCTGGGCCAG	526
QY	62	CTGTGTGAGATTGTGCGCCAAAGTACAGAGGGACCACATGGGGAGTNCNTGTNTGAATCC	121
Db	527	CTGTGTGAGATTGTGCGCCAAAGTACAGAGGGACCACATGGGGAGTTCGTGTCTGAGTCC	586
QY	122	CGNAAGCTCANCNCANCTGCTCCTACTGNACNAGTTCAGNACTGNTGACCTTNGA	181
Db	587	CGTAAGCTCAGCGTCCAGCTGCTCTACTGTACGGTGTTCAGGGACTGCTGACCTTTGA	646
QY	182	TACCTAGTGTGCTGTGCCCATGTNNGANCNATGGCCATGNACATGCGGAAAGCCCTT	241
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QY	242	TTCACTCCCTGCTCCGGCAAGACATTCCTTTNTTTGATGCCAAAAGA CAGGCGAGCGT	301
Db	707	TTCACTCCCTGCTCCGGCAAGACATTCCTTTNTTTGATGCCAAAAGA CAGGCGAGC-T	765
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DEFINITION	AK014319 2676 bp mRNA linear HTC 03-APR-2004
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	enriched library, clone:3222401P09 product:ATP-binding cassette,
	sub-family B (MDR/TAP), member 8, full insert sequence.
ACCESSION	AK014319
VERSION	AK014319.1 GI:12852089
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
	Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
PUBMED	10349636
REFERENCE	2

AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
TITLE	Itch, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to
PUBMED	prepare full-length cDNA libraries for rapid discovery of new genes
REFERENCE	genome Res. 10 (10), 1617-1630 (2000)
AUTHORS	11042159
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	Shibata, K., Itch, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
	Kono, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itch, M.,
	Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
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	Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
	Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN Integrated sequence analysis (RISA) system--384-format
JOURNAL	sequencing pipeline with 384 multicapillary sequencer
PUBMED	genome Res. 10 (11), 1757-1771 (2000)
REFERENCE	11076861
AUTHORS	4
	The RIKEN Genome Exploration Research Group Phase II Team and the
	PANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
REFERENCE	5
AUTHORS	The PANTOM Consortium and the RIKEN Genome Exploration Research
	Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation
JOURNAL	of 60,770 full-length cDNAs
REFERENCE	Nature 420, 563-573 (2002)
AUTHORS	6 (bases 1 to 2676)
	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,

TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshinori Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT Please visit our web site (<http://genome.gsc.riken.jp/>) for further

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGGATCCAGAGCTCTTTTTTTTTTTTIVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTATTAATTAATTCACCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI, 3' end: SstI. Host: SOLR.

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/note="putative"

Query Match	88.7%;	Score 415;	DB 4;	Length 2676;
Best Local Similarity	91.9%;	Pred. No. 3.1e-107;		
Matches 429;	Conservative	0;	Mismatches 37;	Indels 1;
				Gaps 1;

[illegible]

RESULT 8	AK030624	LOCUS	AK030624	2779 bp	mRNA	linear	HTC 03-APR-2003
DEFINITION	Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:530439A07 product:ATP-binding cassette, sub-family B (MDR/TAP), member 8, full insert sequence.						
ACCESSION	AK030624						

VERSION	AK030624.1 GI:26326616
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
AUTHORS	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 11042159
TITLE	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 11076861
JOURNAL	4 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
PUBMED	5 The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 2779)
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/. Location/Qualifiers 1..2779
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polya_site 2779

ORIGIN

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Best Local Similarity 91.9%; Pred. No. 3.2e-107;
Matches 429; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

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DB	587	CGTAAGCTCAGCGTCCAGCTGCTCTACTGACGGTGTTCAGGACTGACCTTGA	646
QY	182	TACCTAGTGTCTGTCCACATTGNNGANCATGGCCATGNACATCGGAAAGCCCTT	241
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CA945430
LOCUS
DEFINITION
CA945430
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 780)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: PYX-5.
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FEATURES

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Site 2: Not I; The library was constructed according to
Bonafido, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into PYX-Aac vector. The library tag
sequence located between the Not I site and the polyA
tail, is TGAGAGAGCC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institutes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 88.5%; Score 414; DB 6; Length 780;
Best Local Similarity 91.6%; Pred. No. 4.5e-107;
Matches 428; Conservative 0; Mismatches 38; Indels 1; Gaps 1;

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DB	240	CTGGTGAGATTGTCCCAAGTACACGAGGACCATGGGAGTTTCTGTCTGAGTCC	299
QY	122	CGNAGCTCANGNCANCTGCTCTACTGNACNGAGTTCAGNACTGNTGACCTTNGA	181
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OY		302 AGTAGTGGCTTGACTACTGATGTGCAAGATTCAAGGCATCCTTNAAGCTTGTCATNTN					361
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ACCESSION	AK076315						
VERSION	AK076315.1	GI:26345291					
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SOURCE	Mus musculus (house mouse)						
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REFERENCE							
AUTHORS	1 Carninci, P. and Hayashizaki, Y.						
TITLE	High-efficiency full-length cDNA cloning						
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)						
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AUTHORS	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.						
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes						
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)						
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AUTHORS	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.						
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer						
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)						
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AUTHORS	4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.						
TITLE	Functional annotation of a full-length mouse cDNA collection						
JOURNAL	Nature 409, 685-690 (2001)						
REFERENCE							
AUTHORS	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.						
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs						
JOURNAL	Nature 420, 563-573 (2002)						
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AUTHORS	6 (bases 1 to 2699)						
	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.						

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 Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
 Muramatsu,M. and Hayashizaki,Y.
 Direct Submission
 Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
 URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
 Fax:81-45-503-9216)
 COMMENT
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 please visit our web site for further details.
 URL:http://genome.gsc.riken.jp/
 URL:http://fantom.gsc.riken.jp/.
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/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP library."

ORIGIN

Query Match 83.9%; Score 392.8; DB 2; Length 771;
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DB 555 CCAGGAGCTGNGCAGCTGNACCCAGGTGATTGTAGCCTGAGAGTGTCTGTATGCTGTC 614
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CF726195

LOCUS UI-M-GZO-cjp-h-06-0-UI.r1 NIH BMAP_GZO Mus musculus cDNA clone
DEFINITION IMAGE:30606413 5', mRNA sequence.

ACCESSION CF726195 GI:37600363

VERSION CF726195
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 750)
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

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Seq primer: PYX-5.
Location/Qualifiers
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/note="Organ: Eye; Vector: pYX-Abs; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Abs vector. The library tag
sequence located between the Not I site and the polyA tail
is TTATTGAGT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

Query Match 70.3%; Score 329.2; DB 6; Length 750;
Best Local Similarity 90.5%; Pred. No. 7.8e-83;
Matches 342; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

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QY 331 AATTCAAGCATCCTTNAAGCTTGTCAATNTNCCAGGAGCTGNGCAGCTGNACCCAGGTGA 390
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QY 391 TTGCTAGCTGAGAGNCCCTGNNATAGCTGNCCTCGCTTACCCTGATGCTGGCTGNNG 450
DB 300 TTGCTAGCTGAGAGTGTCCCTGTCTATGCTGTCCCTCGCTTACCCTGATGCTGGCTGTGG 359
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BI738314

LOCUS 603361553F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5368788 5',
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ACCESSION BI738314 GI:15715314

VERSION BI738314
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 628)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
plate: LHAM1938 row: 1 column: 13
High quality sequence stop: 628.

FEATURES

Source

1. 628
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/clone="IMAGE:5368788"
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/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH MGC 94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

ORIGIN

Query Match 68.6%; Score 321.2; DB 3; Length 628;
Best Local Similarity 90.6%; Pred. No. 1.5e-80;
Matches 345; Conservative 0; Mismatches 34; Indels 2; Gaps 2;
QY 88 GAGGGACCATGGGAGAGTNTGTTGANTCCCGNAGCTCANGNCCANCTGCTCT 147
Db 1 GAGGGACCATGGGAGAGTTTCGTGTGAGTCCGTAAGCTCAGCTCCAGCTGCTCT 60
QY 148 ACTGNACGAGTTGAGNACTGNTGACCTTNGATACCTAGTGTCTGTCTCCACATTGN 207
Db 61 ACTGTACGGTGTTCAGGACTGCTGACCTT-GGATACTAGTGTCTGTCTCCACATTGG 119
QY 208 NGANGNCATGGCCATGNAATGGGAAAGCCCTTTTCAAGTCCCTGCTCCGGCAAGACAT 267
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QY 268 TGCTTTNTTGTATGCCAAAAAGACAGGGCAGCGTAGTAGTCGCTTGACTACTGATGTGC 327
Db 180 TGCTTTCTTGTATGCCAAAAAGACAGGGCAGC-TAGTAGAGTCGCTTGACTACTGATGTGC 238
QY 328 AAGAATTCAAGGCATCTTNAAGCTTGTCAATNTNCCAGGAGCTGNGAGCTGNACCCAGG 387
Db 239 AAGAATTCAAGTCATCTTCAAGCTTGTCAATCTCCAGGAGCTGCGAGCTGCACCCAGG 298
QY 388 TGATTGGTAGCCTTGAGNCCCTGNTATAGCTGNCCTCGCTTACCTGATGCTGCTG 447
Db 299 TGATTGGTAGCCTTGATGTCCTGTCCTATAGCTGTCTCCCTGCTTACCTGATGCTGCTG 358
QY 448 NNGNCACACCCGCCCTCATGG 468
Db 359 TCGTCACACCCGCCCTCATGG 379

RESULT 15
CR857093 LOCUS CR857093 4340 bp mRNA linear HTC 12-NOV-2004
DEFINITION Pongo pygmaeus mRNA; cDNA DKFZp469G0617 (from clone DKFZp469G0617).
ACCESSION CR857093
VERSION CR857093.1 GI:55725060
KEYWORDS HTC.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pongo.
1 (bases 1 to 4340)
AUTHORS Ansoorge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
Mewes,H.W., Well,B., Amd,C., Oesanger,A., Fobo,G., Han,M. and
Wiemann,S.

CONSRM The German cDNA Consortium
TITLE Direct Submission
JOURNAL Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuerberg, GERMANY

COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp469G0617) is available at the RZPD Deutsches
Reisourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
<http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp469G0617>
Further information about the clone and the sequencing project is
available at <http://mips.gsf.de/projects/cdna/>.

FEATURES

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/db_xref="taxon:9600"
/clone="DKFZp469G0617"
/issue_type="kidney"
/clone_1ib="469 (synonym: pkid1). Vector pSPORT1_sfi; host
DH10B; sites SfiIA + SfiIB"
/dev_stage="adult"
/note="Atp-binding cassette, sub-family B, member 8,
mitochondrial precursor (Homo sapiens)"
1. 4340
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77. 2233
/gene="DKFZp469G0617"
/codon_start=1
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LTLMLATPALMGVGTLMGSLRKLRSQCQEQIARAMGVADBALGNVRYTAFAMBO
REBRYGAELEACRRAEELRGIALSQGLSNIAFNQVLGTLFIGSLVAGQQLTGG
DLMSFLVASQTVQSRMANLSVLFGQVVRGLSAGAVFEYMAINPCLPLSGGCVPKBO
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PTAGVVMLDGRDLRTLDPSSLRGQVVGFIQSBEVLFGTTIMENIRFGKLEASDEEYVA
AAREANAHBFITSPREGVNTIVGERGTTLSGGQKQRLAIALIKQPTVLILDEATSA
LDASERVRVQEALDRASAGRTVLVIAHRLSTVRGARIIVVMAQDVRWEAGTHERLLKK
GGLVAEILIRQALDAPRTAAPLPKKPEGRPHQHS"

ORIGIN

Query Match 67.9%; Score 317.6; DB 4; Length 4340;
Best Local Similarity 79.1%; Pred. No. 2.5e-79;
Matches 367; Conservative 0; Mismatches 96; Indels 1; Gaps 1;

QY 5 GAGCTGACCTTAGTGGCGGCACTAGTGAATGTGCAGATCCCTTCTCTGGGCGACGCTG 64
Db 482 GTGCTGGCCTTGGGTGGCGGCACTAGTGAATGTACAGATCCCTGCTCTGGGCGACGCTG 541
QY 65 GTGAGATTGTGCCCAAGTACACGAGGAGCAACATGGGAGAGTNTGNTGANTCCGCGN 124
Db 542 GTAGAGATCGTGGCCAAAGTACACGAGGAGCAACGTGGGAGATTTCATGACTGAGTCCGAG 601
QY 125 AAGCTCANGNCANCTGCTCTACTGNAANGAGTTCAAGNACTGNTGACCTTNGATAC 184
Db 602 AATCTCAGACACCACCTGCTTATCTCTATGTGTTCAGAGGACTTCCTGACCTTCGGGATAC 661
QY 185 CTAGTGTGCTGTCTCCACATGNNANGNCATGGCCATGNACATGGGAAAGCCCTTTTC 244

Db 662 CTGGTGTGCTGTGTCCCAATGTTGGCGAGCGCATGGCTGTGACATGCGAGGGCCCTCTTC 721
OY 245 AGTTCCTGTGCTCCGGCAAGACATTGCTTTTNTTGAATGCCAAAAGACAGGGCAGCGTAGT 304
Db 722 AGTTCCTGTGCTCGACAGACATCGCCCTTCTTGATGCCAATAAGACAGGGCAGC-TGGT 780
OY 305 GAGTGGCTTGACTACTGATGTGCAAGAATTCAAGGCATCCTTNAAGCTTGTCAATNTNCA 364
Db 781 GAGCGCTTGACAACTGACGTGCAAGAGTTAAGTCAATCCTTCAAGCTTGTCAATCTCCA 840
OY 365 GGACTGNGCAGCTGNACCAGGTGATTGTAGCCTGGAGNCCCTGNNTATGCTGNCCCC 424
Db 841 GGGGCTGCGAAGCTGCACCCAGGTGGCAGGCTGCTGGTGTCTGTGCAATGCTGTCTAC 900
OY 425 TCGCCTTACCCTGATGCTGGCTGNNGNCAACCCGCCCTCATGG 468
Db 901 ACGCCTCACGCTGTGCTGATGTGCGCCACACCGGCCCTGATGG 944

Search completed: January 20, 2006, 22:22:46
Job time : 3089 secs

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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 20:26:08 ; Search time 162 Seconds
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5135.178 Million cell updates/sec

Title: US-10-327-713-267
Perfect score: 468
Sequence: 1 gactgagctggccttagtg.....ngncacaccgcgcctcatg 468

Scoring table: IDENTITY_NUC
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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
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 - 8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51.8	11.1	1647	3	US-09-902-540-4211 Sequence 4211, Ap
2	51.8	11.1	21330	3	US-09-902-540-1209 Sequence 1209, Ap
3	46.4	9.9	1743	3	US-09-902-540-4073 Sequence 4073, Ap
4	46.4	9.9	24602	3	US-09-902-540-1202 Sequence 1202, Ap
5	40.8	8.7	9164	3	US-09-814-915A-80 Sequence 80, Appl
6	40	8.5	1959	3	US-09-061-764A-4 Sequence 4, Appl
7	40	8.5	2061	3	US-09-061-764A-17 Sequence 17, Appl
8	36.8	7.9	897	3	US-09-303-518D-37 Sequence 37, Appl
9	36.2	7.7	1272	3	US-09-489-039A-2685 Sequence 2685, Ap
10	36.2	7.7	1812	3	US-09-583-110-1526 Sequence 1526, Ap
11	36.2	7.7	1848	3	US-09-107-433-495 Sequence 495, Appl
12	36.2	7.7	7760	3	US-09-961-527-63 Sequence 63, Appl
13	35	7.5	921	3	US-09-902-540-5880 Sequence 5880, Ap
14	35	7.5	9574	3	US-09-902-540-1043 Sequence 1043, Ap
15	34.8	7.4	1800	3	US-09-252-991A-2972 Sequence 2972, Ap
16	34.8	7.4	2133	3	US-09-252-991A-2716 Sequence 2716, Ap
17	34.8	7.4	165651	3	US-09-949-016-13032 Sequence 13032, A
18	34.6	7.4	601	3	US-09-949-002-1787 Sequence 1787, Ap
19	34.6	7.4	601	3	US-09-949-002-5940 Sequence 5940, Ap
20	34.6	7.4	33821	3	US-09-949-002-613 Sequence 613, App
21	34.6	7.4	33822	3	US-09-949-002-737 Sequence 737, App
22	34.4	7.4	1168	3	US-09-227-357-137 Sequence 137, App
23	34.4	7.4	1168	3	US-09-973-278-143 Sequence 143, App
24	34.2	7.3	1266	3	US-09-252-991A-10804 Sequence 10804, A

25	34.2	7.3	1443	3	US-09-252-991A-10228	Sequence 10228, A
26	34.2	7.3	1818	3	US-09-252-991A-10345	Sequence 10345, A
27	34.2	7.3	1974	3	US-09-902-540-8140	Sequence 8140, Ap
28	34.2	7.3	4213	3	US-09-711-619-8	Sequence 8, Appl
29	34.2	7.3	6189	3	US-09-902-540-754	Sequence 754, Appl
30	34.2	7.3	6827	3	US-09-711-619-7	Sequence 7, Appl
31	34.2	7.3	8450	3	US-09-902-540-834	Sequence 834, App
32	33.8	7.2	1800	3	US-09-489-039A-5879	Sequence 5879, Ap
33	33.6	7.2	1995	3	US-09-902-540-9307	Sequence 9307, Ap
34	33.6	7.2	10092	3	US-09-902-540-994	Sequence 994, App
35	33.6	7.2	13637	3	US-09-902-540-1097	Sequence 1097, Ap
36	33.4	7.1	219	3	US-09-107-532A-3135	Sequence 3135, Ap
37	33.4	7.1	601	3	US-09-949-016-157317	Sequence 157317, Sequence 86, Appl
38	33.4	7.1	753	3	US-09-758-759-86	Sequence 4392, Ap
39	33.4	7.1	2486	3	US-09-949-016-4392	Sequence 16134, A
40	33.4	7.1	12061	3	US-09-949-016-16134	Sequence 1, Appl
41	33.4	7.1	109519	3	US-09-758-759-1	Sequence 8803, Ap
42	33.2	7.1	808	3	US-09-902-540-8803	Sequence 6825, Ap
43	33.2	7.1	1272	3	US-09-902-540-6825	Sequence 569, App
44	33.2	7.1	4407	3	US-09-902-540-569	Sequence 1, Appl
45	33.2	7.1	5552	3	US-08-155-888-1	

ALIGNMENTS

RESULT 1
US-09-902-540-4211
Sequence 4211, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 4211
LENGTH: 1647
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-4211

QY	53	CTGGGCCAGCTGTGGAGATTTCGCCAAGTACACGAGGACCAATGAGGAGTNGTNG	112
DB	19	CTGGCCTATCCCGCGCCATTGGCCACTGTGACACGAGCCCTCACCGCGCGACCGG	78
QY	113	TNTGANTCCGNAAGCTCANCNCNCTGCTCTACTGNACNGAGTTCAGNACTGNTG	172
DB	79	TATGTGTGAGACCGGCTGCGATGTGATGCTGCCGTTCACGCGTGCAGGCGATCGCC	138
QY	173	ACCTTNGATACCTAGTGTGCTGTGCCACATTGNNGANCATGGCCATGNACATGCGG	232
DB	139	ATGGCGTGGCATCTTACCTTTCAACCAACGCGGCAACGCGTGTGTCGCGCTGCGC	198
QY	233	AAAGCCCTTTTACGCTCCCTGCTCCGCAAGACATTGCTTTTGTATGCCAAAAAGACA	292
DB	199	AAAGACCTCTTCGCGCGCTGCTGCCAGAGGTGGCTTCTTGATTCGCGCGCACG	258
QY	293	GGCGAGCTAGTGTGCTTGAATGATGTGCAAGATTCAGGATCCTTNAAGCT	352
DB	259	GGCGAGCTACAC-AGCCGGCTCTCTCGGACACCAACCGTCTCGACACCGTACGCGC	317
QY	353	TGTATNTNCCAGGAGACTGNGACGTGNACCAAGTGATTTGTAGCTTGAGNCCCTGNN	412

Db 318 CAACGTGTCCATGATGCTGCGGCTACGTCGTCACGCGCCCTGGCGGCGTGGCGCTGCTGCT 377
QY 413 TATGCTGNCCCTCGCCTTACCCTGATGCTGCTGNNNGNCACACCCGCCCT 463
Db 378 CTACACGTCCGTCAGCTCACGCTGTGATGCTGCGCCGCTCATCCCGCCCGT 428

RESULT 2

US-09-902-540-1209/c
; Sequence 1209, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1209
; LENGTH: 21330
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURES:
; NAME/KEY: unsure
; LOCATION: (1)..(21330)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1209

Query Match 11.1%; Score 51.8; DB 3; Length 21330;
Best Local Similarity 44.0%; Pred. No. 5.3e-05;
Matches 181; Conservative 0; Mismatches 229; Indels 1; Gaps 1;

QY 53 CTGGGCCAGCTGTGAGATTGTGCGCAAGTACAGAGACCACATGGGGAGTNTCNTG 112
Db 18612 CTGGCCTATCCCGCGCATTTGGCAGCCTGTGTGAGACAGGCCCTCAACGCGCGACCGG 18553
QY 113 TGTGANTCCGNAAGCTCAGNCAGNCAGTGTCTCTACTGNACNGAGTTCAGNACTGNTG 172
Db 18552 TATGTGTGACCGGCTGCGATGTGATGCTGCGCGTGTTCACGGTGACAGGCATCGCC 18493
QY 173 ACCTTNGATACCTAGTCTGTGTGCCACATGNNNGANCATGGCCATGNACATGCGG 232
Db 18492 ATGGCGCTGCGCATCTACTTTCACCAACGCCGCGAAGCGCTGTGTGCGGCTGCGC 18433
QY 233 AAAGCCCTTTTCAAGTCTGCTCCGCGAAGACATGCTTTTNTTGAATGCCAAAAAGACA 292
Db 18432 AAGGACCTCTTCGCGCCCTGCTGTCCACAGAGGTGGCTTCTTCGATTCGCGCGCACG 18373
QY 293 GGGCAGCGTAGTAGTGTGCTGACTACTGATGTGCAAGATTCAAGGCATCTTMAAGCT 352
Db 18372 GCGGAGCTCACC-AGCGGCTCTCTCTCGGACACACCGTCTGCAAGACCAACCGTCACGGC 18314
QY 353 TGTCAATNTCCAGGAGTAGNGACAGCTGNACCAAGGTGATTGTAGCTTGAGNCCCTGNN 412
Db 18313 CAACGTGTCCATGATGTGCGCTACGTCTGTCACGGCCCTGGGCGGCTGTGGCTGTGCT 18254
QY 413 TATGCTGNCCCTCGCCTTACCCTGATGCTGCTGNNNGNCACACCGCCCT 463
Db 18253 CTACACGTCCGTCAGCTCACGCTGTGTGATGCTGCGCCGCTCATCCCGCCCGT 18203

RESULT 3
US-09-902-540-4073
; Sequence 4073, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4073
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-4073

Query Match 9.9%; Score 46.4; DB 3; Length 1743;
Best Local Similarity 48.5%; Pred. No. 0.00078;
Matches 127; Conservative 0; Mismatches 134; Indels 1; Gaps 1;

QY 206 GNNGANCATGCGCATGNACATGCGGAAAGCCCTTTTCACTCTCTGCTCCGCGAAGAC 265
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Db 325 ATCGGTTCTTGA-CCAGCAGCGACTGCGGCTCAACGACCGGCTGTCCACTGACAC 383
QY 326 GCAAGATTGAAGCATCCTTNAAGCTTGTATNTNCCAGGACTGNGAGCTGNACCCA 385
Db 384 CGCCCTCATCAGGGCGCGCTCAGTACGACATCGCCATCATGCTCCGACGCAACCA 443
QY 386 GGTATTGTAGCTTGAAGNCCCTGNNNTATGCTGNCCCTGCTTACCTGATGCTGCG 445
Db 444 GTTATTGAGGGCTGCGCTGCTGCTCTTACACCTCGCCCCGATTGACGCTGCTATGCT 503
QY 446 TGNNGNACACCGCCCTCATG 467
Db 504 GCGGCTGTCGCCCGCGTGACG 525

RESULT 4

US-09-902-540-1202
; Sequence 1202, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1202
; LENGTH: 24602
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1202

Query Match 9.9%; Score 46.4; DB 3; Length 24602;
Best Local Similarity 48.5%; Pred. No. 0.0024;
Matches 127; Conservative 0; Mismatches 134; Indels 1; Gaps 1;

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Db 7290 GGTAGCGCATTTGTACGACCTGCGGAGCGGCTGTATCGACCTGTGAGACAGAG 7349
QY 266 ATTGCTTNTTGTATGCCAAAAAGACAGGCGAGCGTAGTGTGCTTACTACTGATGT 325

Db 7350 ATCGCGTCTTGA-CCAGCACCGCACTGGCGGCTCACAGCCGCTGTCCACTGACAC 7408
QY 326 GCAAGATTCAAGGATCCTTNAAGCTTGTCAATNCCAGGACTGNGCAGCTGNACCCA 385
Db 7409 CGCCCTCATCAGGGCGCGTCACTAGACGACATCGCCATCATGCTCCGCAACGCAACAC 7468
QY 386 GGTGATTGTAGCTGAGNCCCTGNTATGTGNCCTCGCTTACCTGTATGCTGGC 445
Db 7469 GTTGATTGAGGCGCTGGCGCTGCTCTACACCTCGCCCGGTGAGCTCGTCATGCT 7528
QY 446 TGNNGNCACACCCGCTCATG 467
Db 7529 GCGGCTCGTCCCCCGTGACG 7550

RESULT 5

US-09-814-915A-80
; Sequence 80, Application US/09814915A
; Patent No. 6750015
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Kathryn
; APPLICANT: Richer, Jennifer
; TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat
; TITLE OF INVENTION: Theteto
; FILE REFERENCE: 2848-39
; CURRENT APPLICATION NUMBER: US/09/814,915A
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 60/214,870
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 9164
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-915A-80

Query Match 8.7%; Score 40.8; DB 3; Length 9164;
Best Local Similarity 43.8%; Pred. No. 0.078;
Matches 126; Conservative 0; Mismatches 162; Indels 0; Gaps 0;

QY 8 CTGGCCTTAGGTGCGGCACTAGTGAATGTGACAGATCCCTTGTCTCTGGGCCAGCTGCTG 67
Db 6523 CTGGCCCACTGGGTGTGTATGAGAACCTTGACCACTGTGCCCCGGGTCTTGTGCGCC 6582
QY 68 GAGATTGTGCGCAAGTACACGAGGACCAATGAGGAGNTGNTGANTCCGNAAG 127
Db 6583 CTGACGAGACCCCAAGACCTTCTGCGCTGAAGGGGAGGCTGAGAGACAGACACTCCAG 6642
QY 128 CTCANCGNCCANCTGCTCTACTGNAACAGTTCAGAGNATGNTGACCTTNGATACCTA 187
Db 6643 GACGGGGCTGACTGACCTACTGAGCTGTGGACTTCTTGACACCCCGGCTTCAAG 6702
QY 188 GTGCTGTGTCCCATATTGNNGANCATGGCCATGACATGCGGAAAGCCCTTTTCAAC 247
Db 6703 GCCTTGTGGTCCACAGGGGTCTCCAGGTTTGCCTTGACAAAGTGGGGGAGACAGGGAGC 6762
QY 248 TCCCTGTCCGCGCAAGACATTGCTTNTTGTATGCCAAAAAGACAGGG 295
Db 6763 CGGAGCCCCAGGTGAGATGTGCGCAGTGAAGAAAAGTGAAGACAGAG 6810

RESULT 6

US-09-061-764A-4
; Sequence 4, Application US/09061764A
; Patent No. 6284879
; GENERAL INFORMATION:
; APPLICANT: Faustman, Denise L
; TITLE OF INVENTION: TRANSPORT ASSOCIATED PROTEIN SPLICE VARIANTS
; TITLE OF INVENTION: AND MODEL FOR IMMUNE DIVERSITY
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates

STREET: 130 Bishop Allen Drive
; City: Cambridge
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/061,764A
; FILING DATE: April 16, 1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Yankwich, Leon R
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: MGH-002.0 US/MHG-1247.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1959 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: synthetic DNA fragment
US-09-061-764A-4

Query Match 8.5%; Score 40; DB 3; Length 1959;
Best Local Similarity 59.8%; Pred. No. 0.07;
Matches 61; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 198 CCCACATTGNNGANCNCATGGCCATGNACATGCGGAAAGCCCTTTTCAAGTCCCTGCTCC 257
Db 644 CCTACACCATGTCTCGAATCAACTTGGGATCCGGAGCAGCTTCTCTCCTCCTGCTGC 703
QY 258 GGCAGACATTGCTTNTTGTATGCCAAAAAGACAGGGCAGC 299
Db 704 GCCAGACCTCGGTTCTTCCAGAGACTAAGACAGGGAGC 745

RESULT 7

US-09-061-764A-17
; Sequence 17, Application US/09061764A
; Patent No. 6284879
; GENERAL INFORMATION:
; APPLICANT: Faustman, Denise L
; TITLE OF INVENTION: TRANSPORT ASSOCIATED PROTEIN SPLICE VARIANTS
; TITLE OF INVENTION: AND MODEL FOR IMMUNE DIVERSITY
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/061,764A
; FILING DATE: April 16, 1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Yankwich, Leon R
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: MGH-002.0 US/MHG-1247.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: synthetic DNA fragment
;
US-09-061-764A-17
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```

Query Match          8.5%; Score 40; DB 3; Length 2061;
Best Local Similarity 59.8%; Pred. No. 0.071;
Matches 61; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
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QY      198 CCCACATTGNNGANCATGGCCATGNACATGCGAAAGCCCTTTTTCAGCTCCCTGCTCC
           |||||
Db       644 CCTACACCATGCTCGAATCACTTGGCGATCCGGAGACAGCTTTCTCTCCCTGCTGC 703
```

```
QY      258 GGCAAGACATGCTTTNTTGTATGCCAAAGAAGACAGGGCAGC 299
           |||||
Db       704 GCCAGAGCCTCGTTCTTCCAGAGACTAAGACAGGGGAGC 745
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RESULT 8

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US-09-303-518D-37
; Sequence 37, Application US/09303518D
; Patent No. 6914131
; GENERAL INFORMATION:
; APPLICANT: Scarlato, Vincenzo
; APPLICANT: Malignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizzi, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Neisserial Antigens
; FILE REFERENCE: CHIR0160
; CURRENT APPLICATION NUMBER: US/09/303,518D
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1098
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
;
US-09-303-518D-37
```

```

Query Match          7.9%; Score 36.8; DB 3; Length 897;
Best Local Similarity 50.0%; Pred. No. 0.46;
Matches 83; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
```

```
QY      181 ATACCTAGTCTGTCTGCCACATTGNNGANCATGGCCATGNACATGCGAAAGCCCT 240
           |||||
Db       707 ATACGGGGGGGGCTTGGCCGCAACCCGATTGGCTGCCCGGCAAGCGGCAATGATG 766

QY      241 TTTCAGCTCCCTGCTCCGGCAAGACATTGCTTTTGTATGCCAAAGAAGACAGGGCAGCG 300
           |||||
Db       767 CCGCGCGCCACCCGCTCCGGCGGAAAAATACTCTATTTCGTGTCCAAATGACGGCAGCG 826

QY      301 TAGTGAAGCTTGAAGTATGATGTGCAAGAAATTCAAGGCATCCTT 346
           |||||
Db       827 GCTTGAGCCAGTTTACGCATGATTGTGACCGAACAACGCGCGCGT 872
```

```

RESULT 9
US-09-489-039A-2685
```

```

; Sequence 2685, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 2685
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
;
US-09-489-039A-2685
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```

Query Match          7.7%; Score 36.2; DB 3; Length 1272;
Best Local Similarity 45.1%; Pred. No. 0.81;
Matches 92; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
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```
QY      64 GGTGAGATTGTCCCAAGTACACAGAGGACACATGGGAGANTNTGTNTGANTCCG 123
           |||||
Db       798 GGGCGCTATCCGGCCGGCTGACAGCGGAGACAGGTTGATGCTGTCCCGACTCAGCACG 857
```

```
QY      124 NAACTCANCNCNCANTGCTCTCTACTGACNAGAGTTACAGNACTGNTGACCTTNGATA 183
           |||||
Db       858 GCCGCCCGGCGAGCCACGCGCTGCGGTGAGACCCATTCAAGACCCGATCATCGACGCTTA 917
```

```
QY      184 CTTAGTGTCTGTCTCCACATTGNNGANCATGGCCATGNACATGCGAAAGCCCTTTT 243
           |||||
Db       918 CTTGGCGGCGCTGCGCGAAGCGCGCTTGGCGCGGATCTCGCTCGCGACAGCCTTGT 977
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QY      244 CAGCTCCCTGCTCCGCGCAAGACAT 267
Db       978 CGCCGACAGTCAAGCCACGCGCT 1001
```

RESULT 10

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US-09-583-110-1526
; Sequence 1526, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 1526
; LENGTH: 1812
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
;
US-09-583-110-1526
```

```

Query Match          7.7%; Score 36.2; DB 3; Length 1812;
Best Local Similarity 46.6%; Pred. No. 0.95;
Matches 115; Conservative 0; Mismatches 131; Indels 1; Gaps 1;
```

```
QY      129 TCANCNCNCNCCTCTCTACTGNAGAGTTCAAGNACTGNTGACCTTNGATACCTAG 188
           |||||
Db       248 TCATGTCAATCTTGGCCTGTGTTGTTGTTCTATTATCTCTAGTATATACATGT 307

QY      189 TGCTGTGTCCACATTGNNGANCATGGCCATGNACATGCGAAAGCCCTTTTACCT 248
           |||||
```

Db 308 GTCTCATGACGCGCGTGATTGCAGAAATCGAACGAGATGCGCAAGGCCCTTTGGTA 367
QY 249 CCCTGCTCCGGCAGACATTGCTTTTNTTGATGCCAAAAGACAGGCGACGCTAGTAGT 308
Db 368 AGCTTGCTCAGTTGACGGTTTCTTCTTTGA-CCGTGACAAGATGGCGATATCCTGTCT 426
QY 309 CGCTTGACTGATGTGCAAGAATTCAGGCACTCTNAAGCTTGTCATNTNCAGGA 368
Db 427 CATTTACCAAGTGAATTGGATAATATCCTACAGCCTTTAAGAAAGCTTGATTGAGTCT 486
QY 369 CTGNGCA 375
Db 487 ATGAGCA 493

RESULT 11

US-09-107-433-495
; Sequence 495, Application US/09107433
; Patent No. 6800744

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE

FOR DIAGNOSTIC THERAPEUTICS

NUMBER OF SEQUENCES: 5206

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: <Unknown>

OPERATING SYSTEM: <Unknown>

SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/ 085131

FILING DATE: May 12, 1998

APPLICATION NUMBER: 60/051553

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 495:

SEQUENCE CHARACTERISTICS:

LENGTH: 1848 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Streptococcus pneumoniae

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...1848

SEQUENCE DESCRIPTION: SEQ ID NO: 495:

US-09-107-433-495

Query Match 7.7%; Score 36.2; DB 3; Length 1848;
Best Local Similarity 46.6%; Pred. No. 0.95;
Matches 115; Conservative 0; Mismatches 131; Indels 1; Gaps 1;

QY 129 TCANCGNCANCTGCTCCTACTGNACNGAGTTCAGNACTGNATGACCTTNGATACCTAG 188
Db 284 TCATGTCATCTTGGCCCTGCTGTTTGGTCTATTTATCTCTAGTATATACATGT 343
QY 189 TGCTGCTGCCACATTGNNGANCATGGCCATGNACATGCCGAAAGCCCTTTCAAGT 248
Db 344 GTCTCATGACGCGCGTGATTGACAAATCGAACGAGATGCCGAAAGCCCTTTGGTA 403
QY 249 CCCTGCTCCGGCAGACATTGCTTTTNTTGATGCCAAAAGACAGGCGACGCTAGTAGT 308
Db 404 AGCTTGCTCAGTTGACGGTTTCTTCTTTGA-CCGTGACAAGATGGCGATATCCTGTCT 462
QY 309 CGCTTGACTGATGTGCAAGAATTCAGGCACTCTNAAGCTTGTCATNTNCAGGA 368
Db 463 CATTTACCAAGTGAATTGGATAATATCCTACAGCCTTTAAGCAAGCTTGATTGAGTCT 522
QY 369 CTGNGCA 375
Db 523 ATGAGCA 529

RESULT 12

US-08-961-527-63

; Sequence 63, Application US/08961527

; Patent No. 6420135

GENERAL INFORMATION:

APPLICANT: Charles Kunesch

TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences

NUMBER OF SEQUENCES: 391

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961,527

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brookes, A. Anders

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PB340P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 63:

SEQUENCE CHARACTERISTICS:

LENGTH: 7760 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-961-527-63

Query Match 7.7%; Score 36.2; DB 3; Length 7760;
Best Local Similarity 46.6%; Pred. No. 1.8;
Matches 115; Conservative 0; Mismatches 131; Indels 1; Gaps 1;

QY 129 TCANCGNCANCTGCTCCTACTGNACNGAGTTCAGNACTGNATGACCTTNGATACCTAG 188
Db 568 TCATGTCATCTTGGCCCTGCTGTTTGGTCTATTTATCTCTAGTATATACATGT 5717
QY 189 TGCTGCTGCCACATTGNNGANCATGGCCATGNACATGCCGAAAGCCCTTTCAAGT 248

Db 5718 GTCTCATGACGCGGTGATTGCAGAATCGAACAGAGATGCGCAAGGCTCTTTGTA 5777
QY 249 CCCTGCTCCGGCAAGACATGCTTTTNTTATGCAAAAAAGACAGGCGAGTAGTAGT 308
Db 5778 AGCTTGCTCAGTGAACGTTTCTTCTTGA-CGCTGACACAGATGGCGATATCCTGCT 5836
QY 309 CGCTGACTACTGATGTGCAAGATTCAGGCATCCTTNAAGCTTGTCAATNTCCAGGA 368
Db 5837 CATTTACCAAGTGAATTTGATATATCTTCCAAGCCTTTAAGCAAGCTTGATTGAGTC 5896
QY 369 CTGNGCA 375
Db 5897 ATGAGCA 5903

RESULT 13

US-09-902-540-5880
; Sequence 5880, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5880
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-5880

Query Match 7.5%; Score 35; DB 3; Length 921;
Best Local Similarity 50.7%; Pred. No. 1.6;
Matches 68; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 31 GAATGTGAGATCCCTTGCTCTGCGCCAGCTGTGAGATTGTGCCAAGTACACGAG 90
Db 243 GGAGGTGTGTCTGTCGCGGGGAGAGACGGGCTGTGCGAAGCTGCGAAGTACGTGG 302
QY 91 GACCAACATGGGAGNTNCTGTNTGANTCCGNAAGCTCANCGNCCANCTGCTCTACT 150
Db 303 GGAGCAGCCGCTGTGTGGCGTGAATCCGAGCCGAGCGCTTGAAGCGCTGTGTGCC 362
QY 151 GNACNGAGTTCAGG 164
Db 363 CCATTGCGTTTCGG 376

RESULT 14

US-09-902-540-1043/c
; Sequence 1043, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1043
; LENGTH: 9574
; TYPE: DNA

; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(9574)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1043

Query Match 7.5%; Score 35; DB 3; Length 9574;
Best Local Similarity 50.7%; Pred. No. 4.5;
Matches 68; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 31 GAATGTGAGATCCCTTGCTCTGCGCCAGCTGTGAGATTGTGCCAAGTACACGAG 90
Db 5507 GGAGGTGTGTCTGTCGCGGGGAGACGGGCTGTGCGAAGCTGCGAAGTACGTGG 5448
QY 91 GACCAACATGGGAGNTNCTGTNTGANTCCGNAAGCTCANCGNCCANCTGCTCTACT 150
Db 5447 GGAGCAGCCGCTGTGTGGCGTGAATCCGAGCCGAGCGCTTGAAGCGGTGTGTGCC 5388
QY 151 GNACNGAGTTCAGG 164
Db 5387 CCATTGCGTTTCGG 5374

RESULT 15

US-09-252-991A-2972
; Sequence 2972, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 2972
; LENGTH: 1800
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2972

Query Match 7.4%; Score 34.8; DB 3; Length 1800;
Best Local Similarity 48.1%; Pred. No. 2.5;
Matches 75; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 130 CANGNCCANCTGCTCTACTGNACNAGTTGAGNACTGNTGACCTTNGATACCTAGT 189
Db 234 CATCTGTGTTCTTCTGCTGTGCTGCGCTGCGCTGCGCGGCACTTGTGCGCTTCTA 293
QY 190 GCTGCTGTCCCATGTGNNGANCATGGCCATGATGATGCGGAAAGCCCTTTGAGCTC 249
Db 294 CTTGTGTCTGATCGGAGCGCTTGTGCGCGATATCCGCAAGCGGTGTTCAGCA 353
QY 250 CTTGCTCCGGAAGACATTGCTTTTNTTATGACCA 285
Db 354 CTTGATGAGTTGATCCCGGTTTCTACGAAACCA 389

Search completed: January 20, 2006, 22:25:29
Job time : 165 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: January 20, 2006, 20:33:00 ; Search time 657 Seconds
(without alignments)
5890.516 Million cell updates/sec

Title: US-10-327-713-267
Perfect score: 468
Sequence: 1 gactgagctgsccttagtg.....ngncacaccgcctcatg 468

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: '9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:*

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9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	316	67.5	2392	6	US-10-108-260A-258 Sequence 258, App
2	316	67.5	2417	3	US-09-823-245A-601 Sequence 601, App
3	219.6	46.9	1805	6	US-10-264-237-516 Sequence 516, App
4	206.8	44.2	494	3	US-09-918-995-30941 Sequence 30941, A
5	127.8	27.3	423	5	US-10-079-623-212 Sequence 212, App
6	127.8	27.3	423	6	US-10-263-828-64 Sequence 64, App
7	117.6	25.1	425	3	US-09-918-995-34259 Sequence 34259, A
8	93	19.9	2379	10	US-11-097-143-2507 Sequence 2507, App
9	93	19.9	4940	10	US-11-097-143-2506 Sequence 2506, App
10	74	15.8	283	3	US-09-764-891-2676 Sequence 2676, App
11	74	15.8	283	5	US-10-091-572-214 Sequence 214, App
12	55.4	11.8	574	6	US-10-264-237-718 Sequence 718, App
13	51.8	11.1	1773	6	US-10-369-493-43142 Sequence 43142, A
14	46.4	9.9	1773	6	US-10-369-493-43123 Sequence 43123, A
15	44	9.4	434	8	US-10-357-930-30101 Sequence 30101, A
16	44	9.4	483	8	US-10-357-930-45584 Sequence 45584, A
17	40.8	8.7	607	5	US-10-123-155-344 Sequence 344, App
18	40.8	8.7	607	6	US-10-146-731-344 Sequence 344, App
19	40.8	8.7	607	6	US-10-140-472-344 Sequence 344, App
20	40.8	8.7	607	6	US-10-141-761-344 Sequence 344, App
21	40.8	8.7	607	6	US-10-142-885-344 Sequence 344, App
22	40.8	8.7	607	6	US-10-158-790-344 Sequence 344, App
23	40.8	8.7	607	6	US-10-137-871-344 Sequence 344, App

C	24	40.8	8.7	607	6	US-10-140-923-344	Sequence 344, App
C	25	40.8	8.7	607	6	US-10-141-756-344	Sequence 344, App
C	26	40.8	8.7	607	6	US-10-141-759-344	Sequence 344, App
C	27	40.8	8.7	607	6	US-10-140-805-344	Sequence 344, App
C	28	40.8	8.7	607	6	US-10-140-864-344	Sequence 344, App
	29	40.8	8.7	9104	8	US-10-741-600-799	Sequence 799, App
	30	40.8	8.7	9164	7	US-10-776-827-80	Sequence 80, App
	31	40.8	8.7	9272	8	US-10-723-860-1784	Sequence 1784, App
	32	40.8	8.7	9272	9	US-10-956-157-343	Sequence 343, App
	33	40.8	8.7	9277	8	US-10-741-600-801	Sequence 801, App
	34	40.8	8.7	9287	3	US-09-960-706-633	Sequence 633, App
	35	40.8	8.7	9287	3	US-09-873-319-396	Sequence 396, App
	36	40.8	8.7	9456	8	US-10-723-860-6147	Sequence 6147, App
	37	40.2	8.6	455	3	US-09-918-995-208	Sequence 208, App
C	38	39.6	8.5	3450	5	US-10-027-632-116105	Sequence 116105, App
C	39	39.6	8.5	3450	6	US-10-027-632-116105	Sequence 116105, App
	40	38	8.1	1352	8	US-10-739-930-5383	Sequence 5383, App
	41	37.2	7.9	70	9	US-10-957-432-11	Sequence 11, App
	42	37	7.9	506	4	US-09-925-065A-802745	Sequence 802745, App
	43	37	7.9	506	4	US-09-925-065A-802815	Sequence 802815, App
C	44	37	7.9	537	4	US-09-925-065A-805460	Sequence 805460, App
C	45	37	7.9	614	4	US-09-925-065A-857856	Sequence 857856, App

ALIGNMENTS

RESULT 1
US-10-108-260A-258
; Sequence 258, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/10/108, 260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 258
; LENGTH: 2392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-258

Query Match 67.5%; Score 316; DB 6; Length 2392;
Best Local Similarity 78.9%; Pred. No. 7.1e-96;
Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

QY	5	GAGCTGGCTTAAAGTGGCGGCACTAGTGAATGTGCAGATCCCTTGCTCTGGGCGGCACTG	64
DB	428	GTGCTGGCTTGGGTGGCGGCACTGTGAATGTACAGATCCCTTGCTCTGGGCGGCACTG	487
QY	65	GTGAGATTGTGCGCAAGTACAGAGGAGCACACATGGGAGNTNCTGTTGANTCCGN	124
DB	488	GTAGAGGTGTGGCCAGTACAGAGGAGCACAGTAGGAGTTTCATGACTGAGTCCAG	547
QY	125	AAGCTCAGNCNCANCTGCTCTACTGNACNGAGTTGAGNACTGNTGACCTTNGATAC	184
DB	548	AATCTCAGACCCACCTGCTTATCTATGTGTCCAGGACTGTGACCTTGGGTAC	607
QY	185	CTAGTGTGCTGTCCACATTTGNNCNCATGGCCATGNACATGGCGAAGCCCTTTC	244
DB	608	CTGTTGCTGTGTCCACGTTGGCCAGCCATGGCTGTGACATGGGAGGCCCTTTC	667
QY	245	AGCTCCCTGCTCGGCAAGACATTTGTTTGTGATGCCAAAGACAGGCGGCTTACT	304
DB	668	AGCTCCCTGCTCGGCAAGACATCTTCTTGAAGCAAGGAGGAGGCTTACT	726
QY	305	GAGTCGCTTGACTAGTGTGCAAGATTCAGAGGATCTTNAAGCTTGTATNTNCA	364
DB	727	GAGCCGCTTGAACAAGTGCAGGAGTTAAGTCATCTTCAAGCTTGTATCTCCA	786

US-09-918-995-30941
; Sequence 30941, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30941
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(494)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-30941

Query Match 44.2%; Score 206.8; DB 3; Length 494;
Best Local Similarity 80.1%; Pred. No. 3.7e-59;
Matches 229; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 5 GAGCTGGCCTTAAGTGGCGCACTAGTGAATGTGCAATCCCTTGTCTCCGGCCAGCTG 64
|||
DB 208 GTGCTGGCCTTGGGTGGCGCACTGTGAATGTACAGATCCCTGTCTCCGGCCAGCTG 267
65 GTGAGATTGTGCGCAAGTACAGAGGACCAATGGGAGTNCNTGTTGANTCCCGN 124
|||
DB 268 GTAGAGGTGTGGCCAAAGTACAGAGGACCAAGTGGAGTTTCATGACTGAGTCCAG 327
QY 125 AAGCTCAGNCNCANCTGTCTACTGACGAGTTCAAGNACTGNTGACCTTNGGATAC 184
|||
DB 328 AATCTAGCAACCACTGTATCTTATCTTATGTGTCCAGGACTGTGACCTTCCGGTAC 387
QY 185 CTAGTGTCTGTCCACATGNGNANCAATGACATGCGAAAGCCCTTTTC 244
|||
DB 388 CTGTGTCTGTCTCCACGTTGGGAGCGCATGGCTGTGACATGCGAGGCGCTTCTTC 447
QY 245 AGCTCCCTGTCTCCGCAAGACATGCTTTTNTTGTATGCCAAAAGA 290
|||
DB 448 AGCTCCCTGTCTCCGCAAGACATGCTTTTGTGACGCCCAATAAGA 493

RESULT 5
US-10-079-623-212
; Sequence 212, Application US/10079623
; Publication No. US20020169302A1
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; TITLE OF INVENTION: Compositions isolated from bovine
; TITLE OF INVENTION: mammary gland and methods for their use.
; FILE REFERENCE: 11000.1044c3
; CURRENT APPLICATION NUMBER: US/10/079,623
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 212
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Bovine
US-10-079-623-212

Query Match 27.3%; Score 127.8; DB 5; Length 423;
Best Local Similarity 72.5%; Pred. No. 2e-32;

Matches 150; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
QY 83 TACACAGGAGCACATGGGAGTNTGNTGANTCCCGNAGCTCAGNCNCANCTG 142
|||
DB 1 TACACAGGAGCACCGGGGTAGCTTCTGACGAGATCCCGAGCTCAGACCCACCTG 60
QY 143 CTCCTACTGNACNAGTTACAGNACTGNTGACCTTNGATACCTAGTGTCTGTCCAC 202
|||
DB 61 CTCCTCTTACGCGCTCCAGGCGCTGTGACCTTCCGGTACCTGTGTCTGTCCGC 120
QY 203 ATGNNGANCAATGGCCATGNACATGCGGAAAGCCCTTTTACGCTCTCTCCGCAA 262
|||
DB 121 ATCGCGAGCGCATGGCGGTGATCTACGAGGCGCTTTCTGCAACTGTCTCCGCAA 180
QY 263 GACATTGCTTTTNTTGTATGCCAAAAG 289
|||
DB 181 GACATCGAGTTCTTGCATGCTAAGAGG 207

RESULT 6
US-10-263-828-64
; Sequence 64, Application US/10263828
; Publication No. US20030138905A1
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; TITLE OF INVENTION: Compositions isolated from bovine
; TITLE OF INVENTION: mammary gland and methods for their use.
; FILE REFERENCE: 11000.1044U1con
; CURRENT APPLICATION NUMBER: US/10/263,828
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Bovine
US-10-263-828-64

Query Match 27.3%; Score 127.8; DB 6; Length 423;
Best Local Similarity 72.5%; Pred. No. 2e-32;
Matches 150; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 83 TACACAGGAGCACATGGGAGTNTGNTGANTCCCGNAGCTCAGNCNCANCTG 142
|||
DB 1 TACACAGGAGCACCGGGGTAGCTTCTGACGAGATCCCGAGCTCAGACCCACCTG 60
QY 143 CTCCTACTGNACNAGTTACAGNACTGNTGACCTTNGATACCTAGTGTCTGTCCAC 202
|||
DB 61 CTCCTCTTACGCGCTCCAGGCGCTGTGACCTTCCGGTACCTGTGTCTGTCCGC 120
QY 203 ATGNNGANCAATGGCCATGNACATGCGGAAAGCCCTTTTACGCTCTCTCCGCAA 262
|||
DB 121 ATCGCGAGCGCATGGCGGTGATCTACGAGGCGCTTTCTGCAACTGTCTCCGCAA 180
QY 263 GACATTGCTTTTNTTGTATGCCAAAAG 289
|||
DB 181 GACATCGAGTTCTTGCATGCTAAGAGG 207

RESULT 7
US-09-918-995-34259
; Sequence 34259, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30

;; PRIOR APPLICATION NUMBER: US/09/235,076
;; PRIOR FILING DATE: 1999-01-20
;; NUMBER OF SEQ ID NOS: 38054
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 34259
;; LENGTH: 425
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-918-995-34259

Query Match 25.1%; Score 117.6; DB 3; Length 425;
Best Local Similarity 77.7%; Pred. No. 5.7e-29;
Matches 146; Conservative 0; Mismatches 41; Indels 1; Gaps 1;

QY 281 GCCAAAAAGACAGGCGCAGCTAGTGCCTTGACTACTGATGCAAGATTCAAGGC 340
DB 2 GCCAATAAGACAGGCGCAGC-TGGTAGCCGCTTGACCACTGACGTCAGAGATTAACTC 60
QY 341 ATCCTTNAAGCTTGTCATNTNCCAGGAGCTGNGAGCTGNACCCAGGTGATTGTAGCCT 400
DB 61 ATCCTTCAAGCTTGTCATCTCCAGGGGCTGCGAAGCTGCACCCAGGTGCGAGCTGCTT 120
QY 401 GGAGNCCCTGNTATGCTGNCCCTCGCCTTACCTGATGCTGGCTGNNGCACACCCGC 460
DB 121 GGTGTCCCTGTGCATGCTGTGACACGCTTACGCTGTGATGATGTGGCCACACACG 180
QY 461 CCTCATGG 468
DB 181 CTTGATGG 188

RESULT 8

US-11-097-143-2507
;; Sequence 2507, Application US/11097143
;; Publication No. US20050208558A1
;; GENERAL INFORMATION:
;; APPLICANT: Venter, J. Craig
;; APPLICANT: et al.
;; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;; FILE REFERENCE: CL000728
;; CURRENT APPLICATION NUMBER: US/11/097,143
;; CURRENT FILING DATE: 2005-04-04
;; PRIOR APPLICATION NUMBER: 60/157,832
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: 60/160,191
;; PRIOR FILING DATE: 1999-10-19
;; PRIOR APPLICATION NUMBER: 60/161,932
;; PRIOR FILING DATE: 1999-10-28
;; PRIOR APPLICATION NUMBER: 60/164,769
;; PRIOR FILING DATE: 1999-11-12
;; PRIOR APPLICATION NUMBER: 60/173,383
;; PRIOR FILING DATE: 1999-12-28
;; PRIOR APPLICATION NUMBER: 60/175,693
;; PRIOR FILING DATE: 2000-01-12
;; PRIOR APPLICATION NUMBER: 60/184,831
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: 60/191,637
;; PRIOR FILING DATE: 2000-03-23
;; NUMBER OF SEQ ID NOS: 43008
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2507
;; LENGTH: 2379
;; TYPE: DNA
;; ORGANISM: DROSOPHILA
US-11-097-143-2507

Query Match 19.9%; Score 93; DB 10; Length 2379;
Best Local Similarity 53.8%; Pred. No. 2.5e-20;
Matches 179; Conservative 0; Mismatches 153; Indels 1; Gaps 1;
QY 107 TNCNTGNTGANTCCGNAAGCTCANCGNCANCTGCTCTACTGNACNGAGTTGAGNA 166

DB 622 TTCGTAAGACGCTGAGCAACCGGCCAGCAATCTGCTGAGCTTATACATGCTGCATCT 681
QY 167 CTGNTGACCTTNGATATACCTAGTGTCTGTCCACATTGNNGANCATGCGCCATGAC 226
DB 682 GGTTCACCTTTATGTATCATCTTACTGTGTGAGCCGCGGTGAGCAGATGGCAGCCAA 741
QY 227 ATCGGAAGCCCTTTTACGCTCCCTGCTCCGGAAGACATTGCTTTTNTTGAATGCCAA 286
DB 742 ATCGGACGAGATCTGTTACCGCAGATTGTCGTCAGACATGCAATCTTGTGATGAGAA 801
QY 287 AAGACAGGCGCAGCTAGTGTGCTTGACTACTGATGTGCAAGATTCAAGGCATCTT 346
DB 802 CGAACGGCGAGC-TGGTCAATGCACTAACCGCGATGTACAGACTTCAAGACCTCGTT 860
QY 347 NAAGCTTGTCATNTNCCAGGAGCTGNGAGCTGNACCCAGGTGATTGTAGCTGAGNC 406
DB 861 CAAGCAGTTGCTCTCCAGGAGCTGCAAGTGTGCTGCCAGCTGATTGGCGCAGTATATC 920
QY 407 CCGNTATGCTGNCCCTCGCCTTACCTGAT 439
DB 921 GCTCTTCAATGATTTCACCGCAGCATGGCCCAT 953

RESULT 9

US-11-097-143-2506/c
;; Sequence 2506, Application US/11097143
;; Publication No. US20050208558A1
;; GENERAL INFORMATION:
;; APPLICANT: Venter, J. Craig
;; APPLICANT: et al.
;; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;; FILE REFERENCE: CL000728
;; CURRENT APPLICATION NUMBER: US/11/097,143
;; CURRENT FILING DATE: 2005-04-04
;; PRIOR APPLICATION NUMBER: 60/157,832
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: 60/160,191
;; PRIOR FILING DATE: 1999-10-19
;; PRIOR APPLICATION NUMBER: 60/161,932
;; PRIOR FILING DATE: 1999-10-28
;; PRIOR APPLICATION NUMBER: 60/164,769
;; PRIOR FILING DATE: 1999-11-12
;; PRIOR APPLICATION NUMBER: 60/173,383
;; PRIOR FILING DATE: 1999-12-28
;; PRIOR APPLICATION NUMBER: 60/175,693
;; PRIOR FILING DATE: 2000-01-12
;; PRIOR APPLICATION NUMBER: 60/184,831
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: 60/191,637
;; PRIOR FILING DATE: 2000-03-23
;; NUMBER OF SEQ ID NOS: 43008
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2506
;; LENGTH: 4940
;; TYPE: DNA
;; ORGANISM: DROSOPHILA
US-11-097-143-2506

Query Match 19.9%; Score 93; DB 10; Length 4940;
Best Local Similarity 53.8%; Pred. No. 3.3e-20;
Matches 179; Conservative 0; Mismatches 153; Indels 1; Gaps 1;

QY 107 TNCNTGNTGANTCCGNAAGCTCANCGNCANCTGCTCTACTGNACNGAGTTGAGNA 166
DB 3079 TTGTAAGAGCGTGAGCAACCGGCCAGCAATCTGTGAGCTTATACATGCTGCAATCT 3020
QY 167 CTGNTGACCTTNGATATACCTAGTGTGCTGTCCACATTGNNGANCATGCGCCATGNAC 226
DB 3019 GGTTCACCTTTATGTATCATCTTACTGTGAGCCGCGGTGAGCAGATGGCAGCCAG 2960

PRIOR FILING DATE:	2000-09-01
PRIOR APPLICATION NUMBER:	60/229, 345
PRIOR FILING DATE:	2000-09-01
PRIOR APPLICATION NUMBER:	60/229, 287
PRIOR FILING DATE:	2000-09-01
PRIOR APPLICATION NUMBER:	60/229, 513
PRIOR FILING DATE:	2000-09-05
PRIOR APPLICATION NUMBER:	60/231, 413
PRIOR FILING DATE:	2000-09-08
PRIOR APPLICATION NUMBER:	60/229, 509
PRIOR FILING DATE:	2000-09-05
PRIOR APPLICATION NUMBER:	60/236, 367
PRIOR FILING DATE:	2000-09-29
PRIOR APPLICATION NUMBER:	60/237, 039
PRIOR FILING DATE:	2000-10-02
PRIOR APPLICATION NUMBER:	60/237, 038
PRIOR FILING DATE:	2000-10-02
PRIOR APPLICATION NUMBER:	60/237, 038
PRIOR FILING DATE:	2000-10-02
PRIOR APPLICATION NUMBER:	60/236, 370
PRIOR FILING DATE:	2000-09-29
PRIOR APPLICATION NUMBER:	60/236, 370
PRIOR FILING DATE:	2000-09-29
PRIOR APPLICATION NUMBER:	60/236, 802
PRIOR FILING DATE:	2000-10-02
PRIOR APPLICATION NUMBER:	60/237, 037
PRIOR FILING DATE:	2000-10-02
PRIOR APPLICATION NUMBER:	60/237, 040
PRIOR FILING DATE:	2000-10-02
PRIOR APPLICATION NUMBER:	60/240, 960
PRIOR FILING DATE:	2000-10-20
PRIOR APPLICATION NUMBER:	60/239, 935
PRIOR FILING DATE:	2000-10-13
PRIOR APPLICATION NUMBER:	60/239, 937
PRIOR FILING DATE:	2000-10-13
PRIOR APPLICATION NUMBER:	60/241, 787
PRIOR FILING DATE:	2000-10-20
PRIOR APPLICATION NUMBER:	60/246, 474
PRIOR FILING DATE:	2000-11-08
PRIOR APPLICATION NUMBER:	60/246, 532
PRIOR FILING DATE:	2000-11-08
PRIOR APPLICATION NUMBER:	60/249, 216
PRIOR FILING DATE:	2000-11-17
PRIOR APPLICATION NUMBER:	60/249, 210
PRIOR FILING DATE:	2000-11-17
PRIOR APPLICATION NUMBER:	60/226, 681
PRIOR FILING DATE:	2000-08-22
PRIOR APPLICATION NUMBER:	60/225, 759
PRIOR FILING DATE:	2000-08-14
PRIOR APPLICATION NUMBER:	60/225, 213
PRIOR FILING DATE:	2000-08-14
PRIOR APPLICATION NUMBER:	60/227, 182
PRIOR FILING DATE:	2000-08-22
PRIOR APPLICATION NUMBER:	60/225, 214
PRIOR FILING DATE:	2000-08-14
PRIOR APPLICATION NUMBER:	60/235, 836
PRIOR FILING DATE:	2000-09-27
PRIOR APPLICATION NUMBER:	60/230, 438
PRIOR FILING DATE:	2000-09-06
PRIOR APPLICATION NUMBER:	60/215, 135
PRIOR FILING DATE:	2000-06-30
PRIOR APPLICATION NUMBER:	60/225, 266
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PRIOR APPLICATION NUMBER:	60/249, 245
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PRIOR APPLICATION NUMBER:	60/249, 244
PRIOR FILING DATE:	2000-11-17

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2	PRIOR FILING DATE: 2000-11-17
3	PRIOR APPLICATION NUMBER: 60/249, 211
4	PRIOR FILING DATE: 2000-11-17
5	PRIOR APPLICATION NUMBER: 60/249, 215
6	PRIOR FILING DATE: 2000-11-17
7	PRIOR APPLICATION NUMBER: 60/249, 264
8	PRIOR FILING DATE: 2000-11-17
9	PRIOR APPLICATION NUMBER: 60/249, 214
10	PRIOR FILING DATE: 2000-11-17
11	PRIOR APPLICATION NUMBER: 60/249, 297
12	PRIOR FILING DATE: 2000-11-17
13	PRIOR APPLICATION NUMBER: 60/232, 400
14	PRIOR FILING DATE: 2000-09-14
15	PRIOR APPLICATION NUMBER: 60/231, 242
16	PRIOR FILING DATE: 2000-09-08
17	PRIOR APPLICATION NUMBER: 60/232, 081
18	PRIOR FILING DATE: 2000-09-08
19	PRIOR APPLICATION NUMBER: 60/232, 080
20	PRIOR FILING DATE: 2000-09-08
21	PRIOR APPLICATION NUMBER: 60/231, 414
22	PRIOR FILING DATE: 2000-09-08
23	PRIOR APPLICATION NUMBER: 60/231, 244
24	PRIOR FILING DATE: 2000-09-08
25	PRIOR APPLICATION NUMBER: 60/233, 064
26	PRIOR FILING DATE: 2000-09-14
27	PRIOR APPLICATION NUMBER: 60/233, 063
28	PRIOR FILING DATE: 2000-09-14
29	PRIOR APPLICATION NUMBER: 60/232, 397
30	PRIOR FILING DATE: 2000-09-14
31	PRIOR APPLICATION NUMBER: 60/232, 399
32	PRIOR FILING DATE: 2000-09-14
33	PRIOR APPLICATION NUMBER: 60/232, 401
34	PRIOR FILING DATE: 2000-09-14
35	PRIOR APPLICATION NUMBER: 60/241, 808
36	PRIOR FILING DATE: 2000-10-20
37	PRIOR APPLICATION NUMBER: 60/241, 826
38	PRIOR FILING DATE: 2000-10-20
39	PRIOR APPLICATION NUMBER: 60/241, 786
40	PRIOR FILING DATE: 2000-10-20
41	PRIOR APPLICATION NUMBER: 60/241, 221
42	PRIOR FILING DATE: 2000-10-20
43	PRIOR APPLICATION NUMBER: 60/246, 475
44	PRIOR FILING DATE: 2000-11-08
45	PRIOR APPLICATION NUMBER: 60/231, 243
46	PRIOR FILING DATE: 2000-09-08

Query Match	15.84;	Score 74;	DB 5;	Length 283;
Best Local Similarity	77.64;	Pred. No. 2.9e-14;		
Matches 97;	Conservative 1;	Mismatches 26;	Indels 1;	Gaps 1;

OY		242	TTCAGCTCCCTGCTCCGGCAAGACATTGCTTTNTTGTATGC AAAAAGACAGCGCAGCGT	301
		:		
Dδ		219	TTC TTGCCCATG C CAGACAAGACATVACC TTTTGACGCCAATTAGA CAGGCGCAGC -T	161
OY		302	AGTAGTGCCTTGACTACTGATGTGC A GAATTC AAGCAT CCTTNAGCTTGT CATNTN	361
Dδ		160	GGTAGCGCGCTTGACA ACTNACGTG C AGAGATTAA GTCATC CTCAAGCTTGTCATCTC	101
OY		362	CCAGG 366	
Dδ		100	CCAGG 96	

RESULT 12
US-10-264-237-718
; Sequence 718, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237


```
/ APPLICANT: Endege, Wilson
/ APPLICANT: Monahan, John
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
/ TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
/ TITLE OF INVENTION: HUMAN PROSTATE CANCER
/ FILE REFERENCE: MRI-007BCN
/ CURRENT APPLICATION NUMBER: US/10/357,930
/ CURRENT FILING DATE: 2003-02-04
/ PRIOR APPLICATION NUMBER: 09/785,276
/ PRIOR FILING DATE: 2003-02-16
/ PRIOR APPLICATION NUMBER: 60/183,319
/ PRIOR FILING DATE: 2000-02-17
/ PRIOR APPLICATION NUMBER: 60/189,862
/ PRIOR FILING DATE: 2000-03-16
/ PRIOR APPLICATION NUMBER: 60/207,454
/ PRIOR FILING DATE: 2000-05-25
/ PRIOR APPLICATION NUMBER: 60/211,314
/ PRIOR FILING DATE: 2000-06-09
/ PRIOR APPLICATION NUMBER: 60/219,007
/ PRIOR FILING DATE: 2000-07-18
/ PRIOR APPLICATION NUMBER: 60/255,281
/ PRIOR FILING DATE: 2000-12-13
/ NUMBER OF SEQ ID NOS: 62232
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 30101
/ LENGTH: 434
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-357-930-30101
```

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Query Match          9.4%; Score 44; DB 8; Length 434;
Best Local Similarity 46.3%; Pred. No. 0.00049;
Matches 139; Conservative 0; Mismatches 160; Indels 1; Gaps 1;
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QY 140 CTGCTCCTACTGNACNGAGTTCAGNACTGATGACCTTNGATACCTAGTGTGCTGTCC 199
    |||||
Db 55 CTGTCGTGTGCGCGGTGCTGCGGTGCGCACCGCGCGCTTCTACATGTGTCC 114

QY 200 CACATTGNGANCNCATGGCCATGNACATGCGAAAGCCCTTTACGCTCCCTGCTCCGG 259
    |||||
Db 115 TGGCTGGCGGAGCGGTGACGGCAGACATTCGACGGCGGTCTACGGCCACGTGTGCGC 174

QY 260 CAAGACATTGCTTTNTTGTATGCCAAAAAGACAGGGCAGCGTAGTGTGCTTGACTAC 319
    |||||
Db 175 CAGAGCCCCGAATCTTGAGACCAACCCGAC-CGGGAAGTGTGTGCGGCTGACCAAC 233

QY 320 TGATGTGCAAGATTCAAGGCATCCTTNAAGCTTGTCAATNTCCAGGACTGNGCAGCTG 379
    |||||
Db 234 CGACACCAACCCGTGATCCAGACCGTGTGCGGCACCAAGCATCTGCTGGCGCTGCGCAACAC 293

QY 380 NACCCAGGTGATTGTGTAGCTTGAGNCCCTGNNNTATGCTGNCCTGCTTACCTGAT 439
    |||||
Db 294 GCTGCTGTTCTTGGCGGCGCTGTGATGCTGTGTCGACCAAGCCCGGCTGACCTTCAT 353
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Search completed: January 20, 2006, 22:36:34
Job time : 659 secs

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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 20:40:58 ; Search time 242 Seconds
(without alignment)
1594.049 Million cell updates/sec

Title: US-10-327-713-267
Perfect score: 468
Sequence: 1 gactgagctgacctagtg.....ngncacaccgcctcatg 468

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6049916 seqs, 412136615 residues

Total number of hits satisfying chosen parameters: 12099832

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:*

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9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
11: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43.8	9.4	4990	8 US-11-128-061-932	Sequence 932, App
2	43.8	9.4	4990	8 US-11-128-049-932	Sequence 932, App
3	37.8	8.1	2436	8 US-11-128-061-368	Sequence 368, App
4	37.8	8.1	2436	8 US-11-128-049-368	Sequence 368, App
5	36.6	7.8	198285	7 US-10-775-169-338	Sequence 338, App
6	36.2	7.7	201	7 US-10-995-561-68215	Sequence 68215, A
7	36.2	7.7	16175	7 US-10-995-561-13399	Sequence 13399, A
8	35.2	7.5	201	7 US-10-995-561-68325	Sequence 68325, A
9	35	7.5	2446	8 US-11-136-527-3071	Sequence 3071, Ap
10	33.8	7.2	65455	8 US-11-124-368A-2884	Sequence 2884, Ap
11	33.6	7.2	5868	8 US-11-136-527-3354	Sequence 3354, Ap
12	33.4	7.1	2548	8 US-11-136-527-2128	Sequence 2128, Ap
13	33	7.1	1284	7 US-10-750-185-36207	Sequence 36207, A
14	33	7.1	1284	7 US-10-750-623-36207	Sequence 36207, A
15	32.8	7.0	1008	8 US-11-055-822-61	Sequence 61, App1
16	32.6	7.0	3321	8 US-11-136-527-2646	Sequence 2646, Ap
17	32.2	6.9	201	8 US-11-124-368A-5811	Sequence 5811, Ap
18	32.2	6.9	201	8 US-11-124-368A-5812	Sequence 5812, Ap
19	32.2	6.9	201	8 US-11-124-368A-11173	Sequence 11173, A
20	32.2	6.9	201	8 US-11-124-368A-11174	Sequence 11174, A
21	32.2	6.9	503	8 US-11-108-172-878	Sequence 878, App
22	32.2	6.9	4932	8 US-11-124-368A-63	Sequence 63, App1

C 23	32.2	6.9	168656	8 US-11-112-908-59	Sequence 59, App1
C 24	32.2	6.9	170285	8 US-11-112-908-58	Sequence 58, App1
C 25	31.6	6.8	3434	8 US-11-136-527-1894	Sequence 1894, Ap
C 26	31.4	6.7	3497	8 US-11-000-688-1085	Sequence 1085, Ap
27	31.4	6.7	3612	8 US-11-136-527-2282	Sequence 2282, Ap
28	31.4	6.7	4101	7 US-10-821-234-579	Sequence 579, App
29	31.4	6.7	4749	7 US-10-821-234-244	Sequence 244, App
30	31.4	6.7	4770	8 US-11-000-463-7	Sequence 7, App1
31	31.4	6.7	5086	8 US-11-186-284-30	Sequence 30, App1
32	31.4	6.7	5921	8 US-11-186-284-29	Sequence 29, App1
33	31.4	6.7	6728	8 US-11-186-284-27	Sequence 27, App1
34	31.4	6.7	6728	8 US-11-021-603-1	Sequence 1, App1
35	31.4	6.7	26277	7 US-10-995-561-13414	Sequence 13414, A
C 36	31.2	6.7	1400	8 US-11-117-161-10	Sequence 10, App1
C 37	31.2	6.7	1400	8 US-11-080-257-10	Sequence 10, App1
C 38	31.2	6.7	3453	8 US-11-136-527-1893	Sequence 1893, Ap
C 39	30.8	6.6	2026	7 US-10-750-623-44073	Sequence 44073, A
C 40	30.8	6.6	4791	8 US-10-000-463-479	Sequence 479, App
C 41	30.8	6.6	3901	7 US-10-821-234-112	Sequence 112, App
C 42	30.6	6.5	3901	7 US-10-821-234-112	Sequence 112, App
C 43	30.6	6.5	4276	8 US-11-136-527-4010	Sequence 4010, Ap
C 44	30.6	6.5	5460	8 US-11-186-284-32	Sequence 32, App1
C 45	30.6	6.5	6264	8 US-11-075-185-58	Sequence 58, App1

ALIGNMENTS

RESULT 1
US-11-128-061-932
; Sequence 932, Application US/11128061
; Publication No. US20060003958A1

GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; PRIOR FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 932
; LENGTH: 4990
; TYPE: DNA
; ORGANISM: Cricetus griseus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4888)..(4948)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-932

Query Match 9.4%; Score 43.8; DB 8; Length 4990;
Best Local Similarity 46.2%; Pred. No. 0.0017;
Matches 108; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY	5	GAGCTGCTTAAAGTGGCACTAGTGAATGTCAGATCCCTGCTCTGGCCAGCTG	64
DB	1407	GAGAGGCGCTGATGTGCCAAGTGAACGTGAGCTCTGATCTGACTTCGGG	1466
QY	65	GTGAGATTGTGCGCAAGTACGAGGACCATGGGAGNTNCTGTTGANTCCGN	124
DB	1467	GTCTCCCGCTCTCCAGACAGGTGCTCCCTGGCCAGGTTTCCCTGTGCCAG	1526
QY	125	AAGCTCANCNCANCTGCTCTACTGNACNGAGTTGAGNACTGNTGACCTTNGATAC	184

Db 1527 GAATACGGGTCCCAAGGGTGACCGCTGAGAGACTGGATCCAAAGGGGAACAGGGCTTC 1586
QY 185 CTAGTCTGCTGTCTCCACATTGNNGANCATGGCCATGNACATGGGAAAGCC 238
Db 1587 CTGAGAGACGTGGCTTACGAGAGAACCTGGAGCTTGCCGAATGACAGAGAGAC 1640

RESULT 2

US-11-128-049-932

; Sequence 932, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; TITLE OF INVENTION: MAKING AND USING SAME
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 932
; LENGTH: 4990
; TYPE: DNA
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (488)..(4948)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-049-932

Query Match 9.4%; Score 43.8; DB 8; Length 4990;
Best Local Similarity 46.2%; Pred. No. 0.0017;
Matches 108; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 5 GAGCTGGCCTTAGTGGCGCACTAGTAATGTCAGATCCCTTGTCTCTGGCCAGCTG 64
Db 1407 GAGAAAGGCCCTGATGGTCTCCCAAGGTGAACGTGAGAGCTCTGTGATCTTGAGCTTCGGG 1466
QY 65 GTGAGAGATTGTGGCCAAAGTACACAGAGGACCAATGGGAGGAGTNCNTGNTGANTCCCGN 124
Db 1467 GTCTCTCCCGTCTCCAGACAGGTGGTCCCTGGCCAGGGTTTCCCTGTGTTCCAG 1526
QY 125 AAGCTCANGCNCANCTGCTCTACTGNACGAGTTGAGNACTGNTGACCTTNGATAC 184
Db 1527 GAAATACGGGTCCCAAGGTGACCGTGAAGACTGATCCAAAGGGAAACAGGCTTC 1586
QY 185 CTAGTCTGCTGTCTCCCATTTGNNGANCATGGCCATGNACATGGGAAAGCC 238
Db 1587 CTGAGAGACGTGGCTTACGAGAGAACCTGGAGCTTGCCGAATGACAGAGAGAC 1640

RESULT 3

US-11-128-061-368

; Sequence 368, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.

; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 368
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Mesocricetus auratus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (820)..(837)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1544)..(1544)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-368

Query Match 8.1%; Score 37.8; DB 8; Length 2436;
Best Local Similarity 52.4%; Pred. No. 0.094;
Matches 54; Conservative 1; Mismatches 48; Indels 0; Gaps 0;

QY 215 ATGGCCATGNACATCGGAAAGCCCTTTTCAGCTCCCTGCTCCGCAAGACATTGCTTN 274
Db 738 ATCAACCTGCGGATACGGGAGAGGCTTTTCTCCTCTGCTGCGCCAAAGACCTGGGTTT 797
QY 275 TTTGATGCCAAAAGACAGGGCAGCGTAGTGAGTCGCTTGACT 317
Db 798 TTCAGAGAACAGACAGAGGAGGNNNNNNNNNNNNNNNNNGCT 840

RESULT 4

US-11-128-049-368

; Sequence 368, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; TITLE OF INVENTION: MAKING AND USING SAME
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 368
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Mesocricetus auratus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (820)..(837)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1544)..(1544)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-049-368

Query Match 8.1%; Score 37.8; DB 8; Length 2436;
Best Local Similarity 52.4%; Pred. No. 0.094;
Matches 54; Conservative 1; Mismatches 48; Indels 0; Gaps 0;

QY 215 ATGGCCATGNACATGCGGAAAGCCCTTTTACGCTCCCTCGGCAAGACATTGCTTIN 274
DB 738 ATCAACCTGCGATACGGAGAGGCTTTCTCTCTGCTGCGCAAGACCTTGGGTTT 797

QY 275 TTGTATGCCAAAAGACAGGCGACGCTAGTGTGCTTGACT 317
DB 798 TTCCAGAGAGACAGACGAGRGNNNNNNNNNNNNNNNGCT 840

RESULT 5

US-10-775-169-338
; Sequence 338, Application US/10775169
; Publication No. US20050287532A9
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dörner, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 338
; LENGTH: 198285

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-338

Query Match 7.8%; Score 36.6; DB 7; Length 198285;
Best Local Similarity 58.8%; Pred. No. 2.1;
Matches 57; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 198 CCCACATTGNNGANCATGCGCATGNACATGCGGAAAGCCCTTTACGCTCCCTGCTCC 257
DB 118712 CCTACACCATGTCTCGAATCAATTGCGGATCCGGAGAGCACTTTCTCTCTGCTGC 118771

QY 258 GCGAAGACATTGCTTTNTTTGATGCCAAAAGACAGG 294
DB 118772 GCCAGACCTCGGTTTCTTCCAGAGACTAAGACAGG 118808

RESULT 6

US-10-995-561-68215
; Sequence 68215, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68215
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-68215

Query Match 7.7%; Score 36.2; DB 7; Length 201;
Best Local Similarity 57.7%; Pred. No. 0.085;
Matches 56; Conservative 1; Mismatches 40; Indels 0; Gaps 0;

QY 198 CCCACATTGNNGANCATGCGCATGNACATGCGGAAAGCCCTTTTACGCTCCCTGCTCC 257

DB 87 CCTACACCATGTCTGATCACTTGGGATCCGGAGACGCTTTCTCTCTGCTGC 146
QY 258 GCGAAGACATTGCTTTNTTTGATGCCAAAAGACAGG 294
DB 147 GCCAGACCTCGGTTTCTTCCAGAGACTAAGACAGG 183

RESULT 7

US-10-995-561-13399
; Sequence 13399, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13399
; LENGTH: 16175

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13399

Query Match 7.7%; Score 36.2; DB 7; Length 16175;
Best Local Similarity 57.7%; Pred. No. 0.78;
Matches 56; Conservative 1; Mismatches 40; Indels 0; Gaps 0;

QY 198 CCCACATTGNNGANCATGCGCATGNACATGCGGAAAGCCCTTTTACGCTCCCTGCTCC 257
DB 15156 CCTACACCATGTCTGATCACTTGGGATCCGGAGACGCTTTCTCTCTGCTGC 15215

QY 258 GCGAAGACATTGCTTTNTTTGATGCCAAAAGACAGG 294
DB 15216 GCCAGACCTCGGTTTCTTCCAGAGACTAAGACAGG 15252

RESULT 8

US-10-995-561-68325
; Sequence 68325, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68325
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-68325

Query Match 7.5%; Score 35.2; DB 7; Length 201;
Best Local Similarity 62.7%; Pred. No. 0.18;
Matches 52; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 212 CNCATGGCATGNACATGCGGAAAGCCCTTTTACGCTCCCTGCTCCGCAAGACATTGCT 271
DB 8 CGAATCACTTGGGATCCGGAGAGCACTTTCTCTCTGCTGCGCAAGACCTCGGT 67

QY 272 TTNTTGAATGCCAAAAGACAGG 294
DB 68 TTCTTCCAGAGACTAAGACAGG 90

RESULT 9

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US-11-136-527-3071
; Sequence 3071, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3071
; LENGTH: 2446
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3071
```

```
Query Match          7.5%; Score 35; DB 8; Length 2446;
Best Local Similarity 62.4%; Pred. No. 0.72;
Matches 53; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
```

```
QY      215 ATGGCCATGNACATGGCGAAGCCCTTTTCAGCTCCCTGCTCCGGCAGACATTCCTTNN 274
          |||||
Db       750 ATCAACTGCGCATACGAGACAGACGCTTTTCATCTTGTGCGYCAAGACCTTGCAATTC 809

QY      275 TTGATGCCAAAAAGACAGGGCAGC 299
          |||||
Db       810 TTCCAGAGAGACCAAGACAGGGGAGC 834
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RESULT 10

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US-11-124-368A-2884/c
; Sequence 2884, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 2112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2884
; LENGTH: 65455
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-368A-2884
```

```
Query Match          7.2%; Score 33.8; DB 8; Length 65455;
Best Local Similarity 64.1%; Pred. No. 9.1;
Matches 50; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
```

```
QY      267 TTGCTTTNTTGTATGCCAAAGACAGGGCAGCGTAGTGAGTCGCTTGACTAGTATGATGTG 326
          |||||
Db       10263 TTTTITTTTGTAGGTAAAGCTCAGGGAAGCTAAGTCAGTTGCTTGAAAAACAATGTT 10204

QY      327 CAAGAATTCAGGCATCC 344
          |||||
Db       10203 AAAAAGTGAATAGAACCC 10186
```

RESULT 11

```
US-11-136-527-3354
; Sequence 3354, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3354
; LENGTH: 5868
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5416)..(5416)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5439)..(5439)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5858)..(5858)
; OTHER INFORMATION: n is a, c, g, or t
US-11-136-527-3354
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```
Query Match          7.2%; Score 33.6; DB 8; Length 5868;
Best Local Similarity 59.4%; Pred. No. 3.1;
Matches 57; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
```

```
QY      8 CTGGCCTTAGGTGCGGCACTAGTGAATGTCAGATCCCTTGCTCTGGCCAGCTGGTG 67
          |||||
Db       1589 CTGGCAGTCTCTGCGCAGCCCTGTCTCTGATGCGCAAAACCGGCCCTGTCCCGCTGTC 1648

QY      68 GAGATTGTCCGCCAAGTACACGAGGACCAATGGGG 103
          |||||
Db       1649 AAGATGTGCGCCTTGGAACCCGCAAGGTCTCTCTGGAG 1684
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RESULT 12

```
US-11-136-527-2128
; Sequence 2128, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2128
; LENGTH: 2548
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2128
```

```
Query Match          7.1%; Score 33.4; DB 8; Length 2548;
Best Local Similarity 49.6%; Pred. No. 2.4;
Matches 64; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
```

```
QY      65 GTGAGATTGTCCCAAGTACACGAGGACCAATGCGGAGNTNCTGNTGANTCCGNN 124
          |||||
```


Db 1266 GTGGCTACTGTTGGCTACCAAGCCACAGAGCTTTAGGAAATATTGTAGAAATTTGT 1325
Qy 125 AAGCTCANCGNCCANCTGCTCCTACTGACNAGATTCAAGNACTGACTTNGATAC 184
Db 1326 CATCCTGAAGACCAACAACATTCTAAGAGACAGCTTTCAGCAGGTGTGAATTAAAAAGGC 1385
Qy 185 CTAGTGCTG 193
Db 1386 CAAGTGCTG 1394

RESULT 13

US-10-750-185-36207/c
; Sequence 36207, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36207
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Bovine 19866881290303
US-10-750-185-36207

Query Match 7.1%; Score 33; DB 7; Length 1284;
Best Local Similarity 50.7%; Pred. No. 2.2;
Matches 72; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 238 CCTTTTCAGCTCCCTGCTCCGGCAAGACATTGCTTTNTTGTATGCCAAAAAGACAGGGCA 297
Db 554 CCCTTTCAGCTCCATTCTGTGTCAAGAGAAAGCCTTCTTGGGAAACGAATCGACATGGGG 495
Qy 298 GCGTAGTGAGTCGCTTGACTACTGATGTGCAAGAAATTCAGGCAATCCTTNAAGCTTGCA 357
Db 494 CCAGGAGTCAGGCATTGTGTATATGGGGAGGCGAGCCAGCACTGTGTTAGCTTGCC 435
Qy 358 TTNCCAGGAGCTGNGCAGCTG 379
Db 434 CTCCCAAGAGAACACTGACCTG 413

RESULT 14

US-10-750-623-36207/c
; Sequence 36207, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR APPLICATION NUMBER: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36207
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Bovine 19866881290303
US-10-750-623-36207

Query Match 7.1%; Score 33; DB 7; Length 1284;
Best Local Similarity 50.7%; Pred. No. 2.2;
Matches 72; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 238 CCTTTTCAGCTCCCTGCTCCGGCAAGACATTGCTTTNTTGTATGCCAAAAAGACAGGGCA 297
Db 554 CCCTTTCAGCTCCATTCTGTGTCAAGAGAAAGCCTTCTTGGGAAACGAATCGACATGGGG 495
Qy 298 GCGTAGTGAGTCGCTTGACTACTGATGTGCAAGAAATTCAGGCAATCCTTNAAGCTTGCA 357
Db 494 CCAGGAGTCAGGCATTGTGTATATGGGGAGGCGAGCCAGCACTGTGTTAGCTTGCC 435
Qy 358 TTNCCAGGAGCTGNGCAGCTG 379
Db 434 CTCCCAAGAGAACACTGACCTG 413

RESULT 15

US-11-055-822-61
; Sequence 61, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 61
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(985)
; OTHER INFORMATION: KXC00733
US-11-055-822-61

Query Match 7.0%; Score 32.8; DB 8; Length 1008;
Best Local Similarity 45.3%; Pred. No. 2.3;

Matches		91;	Conservative	0;	Mismatches	110;	Indels	0;	Gaps	0;
QY	268	TCCTTNTT	TGATGCCAAAAGACAGGGCAGCGTAGTGCCTTGACTGATGATGCC	327						
Db	609	TGAGCTATT	CGATTCATCAAAACGTGGATCTGCTTAGCCGTGTGACCAACGATGTGG	668						
QY	328	AAGAATTC	AAGGCATCCCTTNAAGCTTGTCAATNCCAGGAGCTGNGCAGCTGNACCAAG	387						
Db	669	ATAATAT	CGGTCAATCCCTGCAACAACCTTGTACAGGCGATCACTTCCCTACTGACCG	728						
QY	388	TGATTGGT	AGCCTGAGNCCCTGNNATGCTGNCCCTCGCCTTACCTGATGCTGGCTG	447						
Db	729	TCATCGGT	GTGTGGATGATGTTATCACTCCCCACTGCTGCGACTCGTGGCGCTGG	788						
QY	448	NNGNCA	CACCCGCGCCTCATGG	468						
Db	789	TATCCAT	TCCGGTCAACATCG	809						

Search completed: January 20, 2006, 22:40:43
Job time : 245 secs